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(57) Abstract

By this invention, methods to produce C14 fatty acids in plant seed oils are provided. In a first embodiment, this invention relates to particular C14 preferring acyl-ACP thioesterase sequences from *Cuphea palustris*, camphor and nutmeg, and to DNA constructs for the expression of these thioesterases in host cells for production of C14 fatty acids. Other aspects of this invention relate to methods for using other plant medium-chain thioesterases or medium-chain thioesterases from non-plant sources to provide C14 fatty acids in plant cells. In this regard, the production of C14 fatty acids in plant cells as the result of expression from *Cuphea palustris*, nutmeg and camphor medium chain acyl-ACP thioesterases is provided.

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PRODUCTION OF MYRISTATE IN PLANT CELLS

This application is a continuation-in-part of USSN 08/383,756 filed February 2, 1995.

Technical Field

The present invention is directed to nucleic acid sequences and constructs, and methods related thereto.

INTRODUCTION

Background

Members of several plant families synthesize large amounts of predominantly medium-chain (C8-C14) triglycerides in specialized storage tissues, some of which are harvested for production of important dietary or industrial medium-chain fatty acids containing oils (F.D. Gunstone, *The Lipid Handbook* (Chapman & Hall, New York, 1986) pp. 55-112). Lauric oil (those containing C12:0 fatty acyl groups) and its derivatives find widespread use, particularly in the soap, detergent and personal care industries.

Over the past several years, mildness has become increasingly important in differentiating soaps, detergents and personal care products, with an emphasis on developing surfactants that combine acceptable performance with improved mildness. Myristate (C14:0) based surfactants offer an excellent combination of cleansing and mildness. However, limitations on the supply of myristate have precluded significant use of these surfactants, despite their functional superiority in certain applications. Myristate is available only in relatively small quantities as a coproduct of the fractionation of lauric oils. Coconut oil contains approximately 48% C12:0 and 17% C14:0, and palm kernel oil contains approximately 51% C12:0 and 18% C14:0. Only a fraction of the C14:0 present in these oils, however, is available as purified C14:0 (myristate), as most commercial "lauric fatty acid/methyl ester" products contain significant amounts of myristate, in addition to the primary laurate

component. Thus, myristate based derivatives currently find only limited use in the personal care product industry due to the high cost involved in their production.

Literature

Pollard, *et al.*, (*Arch. of Biochem. and Biophys.* (1991) *284*:1-7) identified a medium-chain acyl-ACP thioesterase activity in developing oilseeds of California bay, *Umbellularia californica*. The bay thioesterase was subsequently purified by Davies *et al.*, (*Arch. Biochem. Biophys.* (1991) *290*:37-45) which allowed the cloning of a corresponding cDNA which has been used to modify the triglyceride composition of plants (WO 91/16421 and WO 92/20236).

Medium-chain thioesterases from *Cuphea hookeriana* and elm which demonstrated activity on C8 and C10 substrates are described in WO 94/10288. Production of C16 fatty acids in transgenic plants by expression of Class II type thioesterase genes is described in WO 95/13390.

DESCRIPTION OF THE FIGURES

Figure 1. The nucleic acid sequence and translated amino acid sequence of *Cuphea palustris* C14:0-ACP thioesterase cDNA clone MCT34 (CpFatB2) are provided.

Figure 2. The nucleic acid sequence and translated amino acid sequence of a nutmeg (*Myristica fragrans*) Class II type thioesterase, MYRF-1 (MfFatB2), having preferential activity on C14:0-ACP is provided.

Figure 3. The nucleic acid sequence and translated amino acid sequence of a nutmeg (*Myristica fragrans*) Class II type thioesterase, MYRF-2 (MfFatB1), having preferential activity on C14:0-ACP is provided.

Figure 4. Nucleic acid and translated amino acid sequence of a PCR fragment containing the encoding region for the mature protein portion of a camphor Class II acyl-ACP thioesterase is provided.

Figure 5. The nucleic acid sequence and translated amino acid sequence of an elm acyl-ACP thioesterase partial cDNA clone are provided.

Figure 6. The nucleic acid sequence of a *Cuphea hookeriana* CUPH-4 thioesterase cDNA clone, CMT13, is provided.

Figure 7. Nucleic acid sequence of an oleosin expression cassette is provided.

Figure 8. Mole % fatty acid composition data from single seeds of *Brassica* plants 3854-3 and 3854-11, expressing a nutmeg FatB thioesterase, are provided.

Figure 9. Mole % fatty acid composition data from single seeds of *Brassica* plants 5233-5 (Figure 9A) and 5233-6 (Figure 9B), expressing a camphor FatB thioesterase, are provided.

Figure 10. Mole % fatty acid composition data from single seeds of *Brassica* plants 3863-10, 3863-7, 3863-4, 3863-8, 3863-2 and 3863-5 ,expressing a *C. palustris* FatB thioesterase, are provided.

Figure 11. A graph of the C16 and C14 fatty acid compositions of seeds from *B. napus* plants transformed with C14 thioesterases from *C. palustris*, camphor and nutmeg is provided.

Figure 12. Mole % fatty acid composition data from pooled seeds of *Brassica napus* plants transformed with oleosin/*C. palustris* C14 thioesterase (pCGN3864) and oleosin/nutmeg C14 thioesterase (pCGN3857) constructs are provided.

SUMMARY OF THE INVENTION

By this invention, plant genes encoding acyl-ACP thioesterases having the ability to act on C14:0-ACP substrate to form C14:0 (myristate) are provided. Depending on the particular thioesterase employed, the production of myristate may be accompanied by the production of increased proportions of other saturated fatty acids, such as C16 (palmitate) and C18 (stearate). The invention encompasses sequences which encode biologically active thioesterases from plants, as well as sequences which are to be used as probes, vectors for transformation or cloning intermediates. Biologically active sequences are preferentially found in a sense orientation with respect to transcriptional regulatory regions found in various constructs. The instant invention pertains to the entire or portions of the genomic sequence or cDNA sequence and to the

thioesterase protein encoded thereby, including precursor or mature plant thioesterases.

Various plant genes encoding thioesterases having the ability to hydrolyze C14:0-ACP substrate are exemplified herein, and may be obtained for example from *Cuphea* species, nutmeg and camphor. The exemplified plant thioesterase sequences may also be used to obtain other related plant thioesterase genes.

Of special interest are recombinant DNA constructs which can provide for the transcription or transcription and translation (expression) of the disclosed protein sequences. In particular, constructs which are capable of transcription or transcription and translation in plant host cells are preferred. Such construct may contain a variety of regulatory regions including transcriptional initiation regions obtained from genes preferentially expressed in plant seed tissue.

In a second aspect, this invention relates to the presence of such constructs in host cells, especially plant host cells, and to a method for producing proteins having C14 acyl-ACP thioesterase activity in a host cell or progeny thereof via the expression of a construct in the cell. In a related aspect, this invention provides transgenic host cells which have an expressed protein having C14 acyl-ACP thioesterase activity therein.

In a different embodiment, this invention relates to methods of using a DNA sequence encoding a protein having hydrolysis activity on C14:0 acyl-ACP substrates for the modification of the proportion of fatty acids produced within a cell, especially plant cells. Plant cells having such a modified fatty acid composition are also contemplated herein.

Of particular interest is the modification of the fatty acid composition of storage triglycerides in oilseed plants for increased proportion of C14:0 fatty acyl groups, and in some cases, increases in other saturated fatty acyl groups, such as those having 16 and 18 carbons. In this manner, seeds with modified oils having novel fatty acyl compositions are produced. Such novel seeds and oils are also encompassed by the instant invention.

DETAILED DESCRIPTION OF THE INVENTION

A plant protein capable of hydrolyzing C14 acyl-ACP substrates for use in the instant invention includes any sequence of amino acids, peptide, polypeptide or protein which demonstrates the ability to catalyze the production of free fatty acid(s) from C14:0-ACP substrates under plant enzyme reactive conditions. By "enzyme reactive conditions" is meant that any necessary conditions are available in an environment (i.e., such factors as temperature, pH, lack of inhibiting substances) which will permit the enzyme to function. Such proteins having C14 hydrolysis activity are obtainable from various plant sources and will also demonstrate hydrolysis activity on fatty acyl-ACP of varying chain lengths, including such saturated fatty acids as palmitate (16:0) and in some cases, stearate (18:0).

Of particular interest in the instant application are plant acyl-ACP thioesterases which have hydrolysis activity primarily on C14:0-ACP substrates as compared to other acyl-ACP substrates, including medium- or long-chain acyl-ACP substrates. In this regard, thioesterase encoding sequences obtainable from *Cuphea palustris* are of particular interest in the instant invention. Other plant thioesterases having C14:0-ACP activity are also of interest, so long as the thioesterase demonstrates preferential activity on C14:0-ACP substrates, as compared to other medium-chain acyl-ACP substrates, i.e. those having carbon chain lengths of C8, C10 or C12. Thus, acyl-ACP thioesterases from nutmeg and camphor, which have substantial activity on C14:0-ACP substrates, as well as some activity on longer and other medium-chain substrates, are also encompassed by the instant invention. Thus, it is recognized that plant acyl-ACP thioesterases useful for C14 production may also demonstrate hydrolysis activity on longer chain acyl-ACP substrates, such as those having carbon chain lengths of C16 or C18.

In addition to the plant C14:0-ACP thioesterase sequences exemplified herein, acyl-ACP thioesteraes from other plant species are also of interest in the instant invention. Target plant species for isolation of genes encoding thioesterase having activity on C14:0-ACP substrates include those which

have been reported to accumulate significant levels of C14 fatty acids, such as *Myristicaceae*, *Simarubaceae*, *Vochysiaceae*, and *Salvadoraceae*, and rainforest species of *Erisma*, *Picramnia* and *Virola*. For isolating C14:0-ACP thioesterase genes, nucleic acid probes may be prepared from C14:0-ACP thioesterase sequences provided herein, or from other plant medium-chain acyl-ACP thioesterase sequences which have been described.

Plant thioesterases, including medium-chain plant thioesterases are described in WO 91/16421 (PCT/US91/02960), WO 92/20236 (PCT/US92/04332), WO 94/10288 (PCT/US93/10814), and WO 95/13390 (PCT/US94/13131) which are hereby incorporated by reference in their entirety. Analysis of the encoding sequences and translated amino acid sequences of a number of plant acyl-ACP thioesterases has demonstrated the existence of two evolutionary classes of plant acyl-ACP thioesterases which are designated as "Class I" or "FatA" (for fatty acyl transferase type A) and "Class II" (or "FatB"). These classes are not a simple reflection of phylogenetic relationships of the various plants from which the thioesterase encoding sequences were obtained. For example, a *Cuphea hookeriana* FatA clone (clone CLT7 in Figure 10 of WO 94/10288) is closely related to safflower FatA clones (sequences provided in Figure 4 of WO 92/20236). In contrast, a *Cuphea hookeriana* FatB clone (CUPH-1 clone in Figure 6 of WO 94/10288) is equally distant in evolutionary relationship from the *Cuphea hookeriana* FatA clone and the safflower FatA clone.

Class I thioesterases have been found in mango (Fig.1), safflower, *Brassica campestris* and *Cuphea hookeriana*, which sequences are provided in USSN 07/949,102, filed September 21, 1992, now pending, and in WO 92/20236 and WO 94/10288. The plant Class I type thioesterases which have been described to date have preferential activity on longer chain acyl-ACP substrates, particularly 18:1-ACP. Class II thioesterases have been discovered, for example, in California bay, elm, *Cuphea hookeriana*, *Arabidopsis thaliana* and camphor. The plant C14:0 acyl-ACP thioesterases described herein are also of the Class II type. All medium-chain preferring acyl-ACP thioesterases described to date, including those having activity on C14:0, are of the Class II type. Thus, additional plant acyl-ACP

thioesterases having activity on C14:0 substrates may be identified through sequence homology to medium-chain acyl-ACP thioesterases.

For example, a *C. palustris* C14 acyl-ACP thioesterase exemplified herein was obtained by screening a gene library with encoding sequences for medium-chain preferring acyl-ACP thioesterases from *Cuphea hookeriana*. Although the *C. hookeriana* gene sequences encode thioesterases having preferential activity on C8, C10 or C16 fatty acids, the substantial sequence homology within thioesterase genes in various *Cuphea* species allowed for detectable hybridization of the *C palustris* C14 clone to the *C hookeriana* gene probes. For hybridization of C14 thioesterases from plants other than *Cuphea* species, direct hybridization techniques may also be successful under low stringency conditions. For example, nutmeg C14:0-ACP thioesterase clones described herein were obtained by low stringency hybridization screening using a bay C12:0-ACP thioesterase gene fragment as probe. Thus, medium-chain acyl-ACP thioesterase genes from other plant species may be used to identify C14 acyl-ACP thioesterase genes. In addition, highly conserved regions have been identified in various plant medium-chain thioesterase amino acid sequences. Such regions find particular use in identification of additional medium-chain thioesterase genes, including those having preferential activity on C14:0-ACPs, for example by PCR amplification techniques.

As noted above, plants having significant presence of C14:0 fatty acids therein are preferred candidates to obtain naturally-derived C14:0 plant thioesterases. However, it should also be recognized that other plant sources which do not have a significant presence of C14:0 fatty acids may be screened as additional enzyme sources. For example, as discussed herein, a camphor acyl-ACP thioesterase gene was discovered to have preferential hydrolysis activity on C14:0-ACP substrates, with only minor activity on C12:0-ACP substrates, although analysis of camphor seed oil composition indicates significant levels of C12:0 fatty acyl groups and only low levels of C14 fatty acids. Thus, expression of medium-chain acyl-ACP thioesterases in *E. coli* may be used to

identify acyl-ACP thioesterases which find use in production of C14:0 fatty acids in transgenic plant seed oils.

Northern analysis of candidate plant acyl-ACP thioesterase genes may also be useful to identify those having activity on C14:0 fatty acids. In *Cuphea hookeriana*, a clone, CUPH-1, which is expressed at low levels in various plant tissues has been demonstrated to have hydrolytic activity primarily on 16:0 acyl-ACP substrates. A related *C. hookeriana* thioesterase clone, CUPH-2, however, was demonstrated to be highly expressed and seed specific. This CUPH-2 clone was found to have hydrolytic activity primarily on medium-chain acyl-ACP substrates, namely C8 and C10. Similarly, *C. hookeriana* CUPH-4 is highly expressed in a seed specific manner, and as demonstrated further in the Examples herein, may be used to provide for increased production of C14 fatty acids in transformed host cells.

One skilled in the art will readily recognize that antibody preparations, nucleic acid probes (DNA and RNA) and the like may be prepared and used to screen and recover "homologous" or "related" thioesterases from a variety of plant sources. For immunological screening methods, antibody preparations either monoclonal or polyclonal are utilized. For detection, the antibody is labeled using radioactivity or any one of a variety of second antibody/enzyme conjugate systems that are commercially available. Examples of some of the available antibody detection systems are described by Oberfilder (*Focus* (1989) BRL Life Technologies, Inc., *11*:1-5).

For nucleic acid screening methods, genomic or cDNA libraries prepared from a candidate plant source of interest may be probed with conserved sequences from plant thioesterase to identify homologously related sequences. Homologous sequences are found when there is an identity of sequence, which may be determined upon comparison of sequence information, nucleic acid or amino acid, or through hybridization reactions between a known thioesterase and a candidate source. Conservative changes, such as Glu/Asp, Val/Ile, Ser/Thr, Arg/Lys and Gln/Asn may also be considered in determining amino acid sequence homology. Amino acid sequences are considered homologous by as little as 25% sequence identity

between the two complete mature proteins. (*See* generally, Doolittle, R.F., *OF URFS and ORFS* (University Science Books, CA, 1986.)

Typically, a lengthy nucleic acid sequence may show as little as 50-60% sequence identity, and more preferably at least about 70% sequence identity, between the target sequence and the given plant thioesterase of interest excluding any deletions which may be present, and still be considered related. When longer nucleic acid fragments (>100 bp) are employed as probes, such as large cDNA fragments, one may screen with low stringencies (for example 40-50°C below the melting temperature of the probe) in order to obtain signal from the target sample with 20-50% deviation, i.e., homologous sequences. (*See*, Beltz, *et al. Methods in Enzymology* (1983) *100*:266-285.).

Shorter probes are also useful in thioesterase gene isolation techniques, and find particular applications in polymerase chain reactions (PCR). As described in more details in the following examples, medium-chain thioesterase gene fragments may be obtained by PCR using primers to sequences which are highly conserved in plant medium chain acyl-ACP thioesterase protein sequences.

Using methods known to those of ordinary skill in the art, a DNA sequence encoding a protein having hydrolytic activity on C14:0-ACP substrate can be inserted into constructs which may then be introduced into a host cell of choice for expression of the enzyme, including plant cells for the production of transgenic plants. Thus, potential host cells include both prokaryotic and eukaryotic cells. A host cell may be unicellular or found in a multicellar differentiated or undifferentiated organism depending upon the intended use. Cells of this invention may be distinguished by having a protein having hydrolysis activity on C14:0 acyl-ACP substrates foreign to the wild-type cell present therein, for example, by having a recombinant nucleic acid construct encoding a plant thioesterase therein.

Also, depending upon the host, the regulatory regions will vary, including regions from viral, plasmid or chromosomal genes, or the like. For expression in prokaryotic or

eukaryotic microorganisms, particularly unicellular hosts, a wide variety of constitutive or regulatable promoters may be employed. Among transcriptional initiation regions which have been described are regions from bacterial and yeast hosts, such as *E. coli, B. subtilis, Sacchromyces cerevisiae,* including genes such as beta-galactosidase, T7 polymerase, tryptophan E and the like.

For the most part, when expression in a plant host cell is desired, the constructs will involve regulatory regions (promoters and termination regions) functional in plants. The open reading frame, coding for the protein having hydrolytic activity on C14:0-ACP substrate will be joined at its 5' end to a transcription initiation regulatory region such as the wild-type sequence naturally found 5' upstream to a plant thioesterase structural gene. Numerous other transcription initiation regions are available which provide for a wide variety of constitutive or regulatable, e.g., inducible, transcription of the structural gene functions. Among transcriptional initiation regions used for plants are such regions associated with the structural genes such as for CaMV 35S and nopaline and mannopine synthases, or with napin, ACP promoters and the like. The transcription/translation initiation regions corresponding to such structural genes are found immediately 5' upstream to the respective start codons. If a particular promoter is desired, such as a promoter native to the plant host of interest or a modified promoter, i.e., having transcription initiation regions derived from one gene source and translation initiation regions derived from a different gene source, including the sequence encoding the plant thioesterase of interest, or enhanced promoters, such as double 35S CaMV promoters, the sequences may be joined together using standard techniques. For most applications desiring the expression of C14:0-ACP thioesterases in plants, the use of seed specific promoters is preferred.

For some applications, expression of other proteins in conjunction with expression of C14:0-ACP thioesterase may be desired. For example, as described in further detail in the following examples, expression of C14:0-ACP thioesterase results in C14 levels of up to 40 mole percent may be obtained,

analysis of the *sn*-1, 2 and 3 positions of the triglycerides indicates limited incorporation of C14 into the *sn*-2 position. Expression of a medium-chain preferring lysophosphatidic acid acyl transferase (LPAAT) in combination with a C14:0-ACP thioesterase results in increased incorporation of C14 into the *sn*-2 position. A plant medium-chain preferring LPAAT is described in international patent application number PCT/95/03997 (published as WO 95/27791), which is incorporated herein in its entirety.

When expression of the proteins of the instant invention is desired in plant cells, various plants of interest include, but are not limited to, rapeseed (Canola varieties, including low linolenic lines, and High Erucic Acid varieties), sunflower, safflower, cotton, *Cuphea*, soybean, peanut, coconut and oil palms, and corn. Depending on the method for introducing the recombinant constructs into the host cell, other DNA sequences may be required. Importantly, this invention is applicable to dicotyledyons and monocotyledons species alike and will be readily applicable to new and/or improved transformation and regulation techniques.

In any event, the method of transformation is not critical to the instant invention; various methods of plant transformation are currently available. As newer methods are available to transform crops, they may be directly applied hereunder. For example, many plant species naturally susceptible to *Agrobacterium* infection may be successfully transformed via tripartite or binary vector methods of *Agrobacterium* mediated transformation. In addition, techniques of microinjection, DNA particle bombardment, electroporation have been developed which allow for the transformation of various monocot and dicot plant species.

The C14 fatty acids produced in the transgenic host cells of this invention are useful in various commercial applications, and will find particular use, for example, in the detergent industry. Oils containing varying amounts of C14 and C16 fatty acids essentially in the *sn*-1 and *sn*-3 positions may find use in food applications, such as for shortenings.

The following examples are provided by way of illustration and not by way of limitation.

EXAMPLES

Example 1 Acyl-ACP Thioesterase Sequences

A. *Cuphea hookeriana*

DNA sequences corresponding to *Cuphea* thioesterase peptide regions are obtained by PCR using degenerate olgonucleotides designed from peptide fragments from conserved regions of plant thioesterases described in WO 92/20236. A forward primer, TECU9, contains 17 nucleotides corresponding to all possible coding sequences for amino acids 176-181 of the bay and camphor thioesterase proteins. A reverse primer, TECU3A, contains 18 nucleotides corresponding to the complement of all possible coding sequences for amino acids 283-288 of the bay and camphor thioesterase proteins, In addition, the forward and reverse primers contain *Bam*HI or *Xho*I restriction sites, respectively, at the 5' end, and the reverse primer contains an inosine nucleotide at the 3' end. The safflower, bay and camphor sequences diverge at two amino acid positions in the forward primer region, and at one amino acid residue in the reverse primer region. The degeneracy of oligonucleotide primers is such that they could encode the safflower, bay and camphor sequences.

Polymerase chain reaction samples (100µl) are prepared using reverse transcribed *Cuphea hookeriana* RNA as template and 1µM of each of the oligonucleotide primers. PCR products are analyzed by agarose gel electrophoresis, and an approximately 300bp DNA fragment, the predicted size from the thioesterase peptide sequences, is observed. The DNA fragment, designated C93A (*Cuphea*) is isolated and cloned into a convenient plasmid vector using the PCR-inserted *Bam*HI and *Xho*I restriction digest sites. DNA sequence of representative clones is obtained. Analysis of these sequences indicates that at least two different, but homologous *Cuphea hookeriana* cDNAs were amplified.

Total *Cuphea* RNA for cDNA library construction may be isolated from developing *Cuphea hookeriana* embryos by modifying the DNA isolation method of Webb and Knapp (*Plant Mol. Biol. Reporter* (1990) *8*:180-195). Buffers include:

REC: 50mM TrisCl pH 9, 0.7 M NaCl, 10 mM EDTA pH8, 0.5% CTAB.

REC+: Add B-mercaptoethanol to 1% immediately prior to use.

RECP: 50 mM TrisCl pH9, 10 mM EDTA pH8, and 0.5% CTAB

RECP+: Add B-mercaptoethanol to 1% immediately prior to use.

For extraction of 1 g of tissue, 10ml of REC+ and 0.5 g of PVPP is added to tissue that has been ground in liquid nitrogen and homogenized. The homogenized material is centrifuged for 10 min at 1200 rpm. The supernatant is poured through miracloth onto 3ml cold chloroform and homogenized again. After centrifugation, 12,000 RPM for 10 min, the upper phase is taken and its volume determined. An equal volume of RECP+ is added and the mixture is allowed to stand for 20 min. at room temperature. The material is centrifuged for 20 min. at 10,000 rpm twice and the supernatant is discarded after each spin. The pellet is dissolved in 0.4 ml of 1 M NaCl (DEPC) and extracted with an equal volume of phenol/chloroform. Following ethanol preciptation, the pellet is dissolved in 1 ml of DEPC water. Poly (A) RNA may be isolated from this total RNA according to Maniatis *et al.* (*Molecular Cloning: A Laboratory Manual* (1982) Cold Springs Harbor, New York). cDNA libraries may be constructed in commercially available plasmid or phage vectors.

Thioesterase encoding fragments obtained by PCR as described above are labeled and used to screen *Cuphea* cDNA libraries to isolate thioesterase cDNAs. Preliminary DNA sequence of a *Cuphea* cDNA clone TAA 342 is presented in Figure X. Translated amino acid sequence of the *Cuphea* clone from the presumed mature N-terminus (based on homology to the bay thioesterase) is shown.

The sequence is preliminary and does not reveal a single open reading frame in the 5' region of the clone. An open reading frame believed to represent the mature protein sequence is shown below the corresponding DNA sequence. The N-terminal amino acid was selected based on homology to the bay thioesterase protein.

Additional *Cuphea hookeriana* cDNA clones were obtained by screening a cDNA library prepared using a Uni-ZAP (Stratagene) phage library cloning system. The library was screening using radiolabeled TAA 342 DNA. The library was hybridized at 42°C uing 30% formamide, and washing was conducted at low stringency (room temperature with 1X SSC, 0.1% SDS). Numerous thioesterase clones were identified and DNA sequences determined. Three classes of *Cuphea* cDNA clones have been identified. The original TAA 342 clone discussed above is representative of CUPH-1 type clones which have extensive regions of homology to other plant medium-chain preferring acyl-ACP thioesterases. Nucleic acid sequence and translated amino acid sequence of a CUPH-1 clone, CMT9, is shown in Figure 6 of WO 94/10288. The mature protein is believed to begin either at or near the leucine at amino acid position 88, or the leucine at amino acid position 112. Northern analysis of RNA isolated from various *Cuphea hookeriana* plant tissues indicates that the CUPH-1 gene is expressed at a low level in all *Cuphea hookeriana* plant tissues examined.

A second class of *Cuphea* thioesterase cDNAs is identified as CUPH-2. These cDNAs also demonstrate extensive homology to other plant medium-chain acyl-ACP thioesterases. Expression of a representative clone, CMT7, in *E. coli* demonstrated that CUPH-2 clones encode a medium-chain preferring acyl-ACP thioesterase protein having preferential activity towards C8 and C10 acyl-ACP substrates. DNA sequence and translated amino acid sequence of CMT7 is shown in Figure 7 of WO 94/10288.

Preliminary DNA sequence from the 5' end of an additional *Cuphea hookeriana* clone, CMT13, is shown in Figure 6 herein. Although CMT13 demonstrates extensive sequence identity with CMT7, DNA sequence alignment reveals several gaps, which together total approximately 48 nucleotides, where the CMT13 clone is missing sequences present in the CMT7 clone. CMT13 is also referred to as a CUPH-4 clone. Northern analysis of RNA isolated from various *Cuphea hookeriana* plant tissues indicates that CUPH-2 and CUPH-4 genes are highly expressed in developing seed tissues. Expression of the CUPH-2 and CUPH-4 clones in other *C. hookeriana* tissues, such as leaves, was not detected.

DNA sequence of an additional clone, CMT10, is shown in Figure 9 of WO 94/10288. CMT10 has greater than 90% sequence id ntity with CMT9, but less than the approximately 99% sequence identity noted in fragments from other CUPH-1 type clones. CMT10 is also referred to as a CUPH-5 type clone.

B. *Cuphea palustris*

Total RNA is isolated from developing seeds of *C. palustris* as described above for *C. hookeriana*. A lambda ZipLox (BRL; Gaithersburg, MD) cDNA library containing approximately 6 X 10^6 pfu is constructed from total RNA. Approximately 500,000 plaques from the unamplified library are screened using a mixed probe containing the thioesterase coding regions from *Cuphea hookeriana* CUPH-1 (CMT-9), CUPH-2 (CMT-7) and CUPH-5 (CMT-10). (DNA sequences of these clones are provided in WO 94/10288). Low stringency hybridization conditions are used: hybridization is conducted at room temperature in a solution of 30% formamide and 2X SSC (1X SSC = 0.15 M NaCl; 0.015 M Na citrate). Eighty two putative positive clones were identified, thirty of which were plaque purified.

The nucleic acid sequence and translated amino acid sequence of clone designated as MCT34 is provided in Figure 1. The translated amino acid sequence of this clone is approximately 80% identical to the sequence of a *Cuphea hookeriana* CUPH-4 clone (CMT-13 in Figure 8 of WO 94/10288).

C. Nutmeg (*Myristica fragrans*)

Total RNA is isolated from developing nutmeg seeds as described above for *Cuphea* species. A lambda Zap (Stratagene; La Jolla, CA) cDNA library is constructed from total RNA. A *Bam*HI/*Pst*I fragment of pCGN3822 containing approximately 900bp of a bay thioesterase C12 preferring acyl-ACP thioesterase encoding sequence (Figure 1 of WO 94/10288) is radiolabeled and used as a probe of the nutmeg cDNA library under the following hybridization conditions: overnight hybridization at 30°C in 50% formamide, 2X SSC, 5% dextran sulfate. The hybridized filters are washed at 30°C in 0.1% SSC, 0.1%SDS and autoradiographed. Five putative positive clones were identified, thre of which contain the sequence shown in Figure 3, and are designated MYRF-2 or MfFatB1, and one of which contained the sequence shown in Figure 2, and which is

designated MYRF-1 or MfFatB2. Sequence of the other putative positive clone indicated that it did not encode an acyl-ACP thioesterase.

Sequence analysis of the MYRF-1 and MYRF-2 clones indicates that MYRF-1 is substantially a truncated version of MYRF-2, the initial proline residue of MYRF-1 corresponds to amino acid 97 of the MYRF-2 sequence. Another major difference in these clones is seen at the 3' end of the thioesterase encoding regions. The MYRF-1 clone lacks the TAG stop codon at nucleotides 1624-1626 of the MYRF-2 sequence, and thus the translated amino acid sequence of MYRF-1 extends into the MYRF-2 3' untranslated region until the next available in frame stop codon is reached (TGA at nucleotides 1087-1089 of MYRF-1).

D. Camphor (*Cinnamomum camphora*)

DNA sequence and translated amino acid sequence of a Class II camphor thioesterase encoding region generated by PCR is provided in Figure 5B of WO 92/20236. A DNA fragment containing the mature protein region of the camphor clone is obtained by PCR from reverse transcribed cDNA prepared using RNA from developing camphor embryos. Forward (sense) and reverse (antisense) PCR primers, #4164 and #4165, are prepared which contain sequences useful for cloning using the CLONEAMP™ system (GIBCO BRL; Gaithersburg, MD). Oligonucleotide 4164 contains a 20 nucleotide region corresponding to the camphor thioesterase encoding sequence of nucleotides 119-138 of the sequence in Figure 5B of WO 92/20236. Oligonucleotide 4165 contains a 20 nucleotide region complementary to the camphor thioesterase 3' untranslated sequence represented as nucleotides 1391-1410 of Figure 5B in WO 92/20236. The sequences of 4164 and 4165 are as follows:

#4164 5' CUACUACUACUATCGATACCATCTTTTCGGCTGCTGA 3'
#4165 5' CAUCAUCAUCAUGAGCTCGCAAGAGAAAGAGCTTACAG 3'.

DNA sequence and translated amino acid sequence of a camphor PCR fragment obtained by PCR with 4164 and 4165 are provided in Figure 4. The sequence begins at the *Xba*I site located at the b ginning of the mature protein encoding region of the camphor thioesterase.

Example 2 - Expression of C14:0 Acyl-ACP Thioesterases in *E. coli*

A. *Cuphea palustris*

Constructs for expression of a *Cuphea palustris* acyl-ACP thioesterase encoding sequence in *E. coli* are prepared. cDNA clone MCT34 is used as template for a polymerase chain reaction (PCR) to insert a *Stu*I site 5' to the presumed mature protein start site located at amino acid 108 of the sequence shown in Figure 1. A forward primer for PCR, MCT34F1, contains DNA sequence corresponding to nucleotides 437-454 of the *C. palustris* sequence shown in Figure 1, as well as sequences for insertion of *Sph*I and *Stu*I restriction digestion sites. An M13 sequencing primer referred to as "M13 Forward" is used for priming the reverse, or antisense, reaction. Sequence of the PCR primers are as follows:

MCT34F1 5' CUACUACUACUAGAATTCGCATGCAGGCCTATGCTTGACCGGAAATCT 3'
M13 Forward 5' GTTTTCCCAGTCACGAC 3'.

The resulting PCR product is cloned as a *Stu*I/*Xba*I fragment into pUC118, resulting in clone MCT34LZ, which provides for expression of the *C. palustris* thioesterase in *E. coli* as a *lac*Z fusion protein.

An additional construct for expression of the *C. palustris* thioesterase cDNA clone MCT34 in *E. coli* is prepared using a Qiagen (Chatsworth, CA) pQE vector which provides for high level expression and protein purification capability through a histidine tag. The DNA product resulting from PCR using the MCT34F1 and M13 Forward primers described above, is digested with *Sph*I and *Sna*BI and cloned into *Sph*I and *Sma*I digested pQE30 (Qiagen), resulting in MCT34HT.

MCT34LZ is transformed into *E. coli fad*D, an *E. coli* mutant which lacks medium-chain specific acyl-CoA synthetase (Overath *et al.*, *Eur. J. Biochem* (1969) 7:559-574) for analysis of lipid composition. Cells containing the thioesterase construct, and a similar culture of control cells are grown at 30°C to an OD_{600} of ~0.5. Induction of the thioesterase expression may be achieved by the addition of IPTG to 0.2 to

0.4 mM followed by further growth for 30 to 120 minutes. For slow growing cultures, longer growth periods may be required following addition of IPTG. A 4.5ml sample of the *E. coli* cells is transferred into a 15ml glass vial with a teflon-lined cap. 100µl of a 1mg/ml standards solution containing 1mg/ml each of C11:0 free fatty acid, C15:0 free fatty acid, and C17:0 TAG in 1:1 chloroform/methanol is added to the sample, followed by addition of 200µl of glacial acetic acid and 10ml of 1:1 chloroform/methanol. The samples are vortexed to mix thoroughly and centrifuged for 5 minutes at 1000rpm for complete phase separation. The lower (chloroform) phase is carefully removed and transferred to a clean flask appropriate for use in a rotary evaporator (Rotovap). The sample is evaporated to near dryness. As medium-chain fatty acids appear to evaporate preferrentially after solvent is removed, it is important to use just enough heat to maintain the vials at room temperature and not completely remove the chloroform. The liquid residue is measured and transferred to a 2ml glass vial with a Teflon cap. The vial used in the rotary evaporator is washed with chloroform/methanol, and the chloroform/methanol sample is pooled with the liquid residue (total volume of 600µl).

For analysis of total fatty acids, a 100µl aliquot of the sample is methanolyzed by adding 1 ml of 5% sulfuric acid in methanol, transferring the samples to a 5ml vial, and incubating the sample in a 90°C water bath for 2 hours. The sample is allowed to cool, after which 1ml of 0.9% NaCl and 300µl of hexane are added. The sample is vortexed to mix thoroughly and centrifuged at 1000rpm for 5 minutes. The top (hexane) layer is carefully removed and placed in a plastic autosampler vial with a glass cone insert, followed by capping of the vial with a crimp seal.

For analysis of free fatty acids, the following TLC procedure for separation of free fatty acids from phospholipids (Cho and Cronan (1994) *J. Bacterial.* 1793-1795) is applied prior to methanolysis as described above. A 100µl aliquot of the rotary evaporator residue and wash solution described above is applied to two lanes (50µl/lane) of a silica-G TLC plate. The plates are developed in petroleum ether/ether/acetic acid

(70/30/2, v/v) for approximately 15-20 minutes. The phospholipids remain at the origin, while the neutral lipids migrate close to the solvent front. Lipids are stained with iodine very briefly, marked and the silica from the marked areas transfered to Teflon-capped 2ml tubes. The respective areas from the two lanes are pooled, and the samples are methanolyzed as described above.

Samples are analyzed by gas-liquid chromatography (GC) using a temperature program to enhance the separation of components having 10 or fewer carbons. The temperature program used provides for a temperature of 140°C for 3 minutes, followed by a temperature increase of 5°C/minute until 230°C is reached, and 230°C is maintained for 11 minutes. Samples are analyzed on a Hewlett-Packard 5890 (Palo Alto, CA) gas chromatograph. Fatty acid content calculations are based on the internal standards. Results are presented in Table 1 below.

TABLE 1

Free Fatty Acids (nmol/ml) in E. coli (*fadD*)

Strain	12:0	14:0	14:1	16:0	16:1	18:1
Control	1.87	0.54	0.0	1.70	0.0	0.0
MCT34LZ	2.41	8.83	19	2.96	0.0	0.0

The above results demonstrate a substantial increase in the production of 14:0 and 14:1 fatty acids in cells transformed with the *C. palustris* MCT34LZ clone.

B. *C. hookeriana* CUPH-4

A construct for expression of *C. hookeriana* CUPH-4 thioesterase in *E. coli* as a *lac*Z fusion is also prepared using PCR and cloning techniques such as described above for preparation of *C. palustris* constructs.

C. Nutmeg

Constructs for expression of two nutmeg (*Myristica fragrans*) Class II type thioesterases, MYRF-1 (MfFatB2) and MYRF-2 (MfFatB1), in *E. coli* as *lac*Z fusion proteins are prepared. MfFatB1 and MfFatB2 are digested with *Sal*I and *Xho*I

to excise the clone fragments containing the thioesterase encoding sequence from amino acid 131 of the MfFatB1 sequence (Figure 3), or amino acid 35 of the MfFatB2 sequence (Figure 2), through the 3' ends of the cDNA clones. The excised thioesterase encoding fragments are inserted into *SalI* digested pUC8 resulting in pCGN3856 (MfFatB1) and pCGN3855 (MfFatB2). These constructs encode *lacZ* fusions of the approximate mature thioesterase protein sequence (amino acid 130 of the MfFatB1 preprotein was selected as the mature protein N-terminus by homology to bay thioesterase protein).

The fusion proteins are expressed in *fad*$^+$ and *fadD* strains of *E. coli* K12. Analysis of total fatty acids in liquid cultures of MYRF-1 and MYRF-2 transformed K27(*fadD*) after overnight growth at 30°C are provided in Table 2 below.

D. Camphor

The camphor PCR fragment described above is cloned into a pAMP vector resulting in pCGN5219. pCGN5219 is digested with *XbaI* and *SalI* and the resulting camphor thioesterase fragemnt is cloned into *XbaI* and *SalI* digested pBCSK+ (Stratagene), resulting in pCGN5220. pCGN5220 is used to transform *E. coli fadD* for analysis of lipid composition as described above. Results of these analyses are provided in Table 2 below.

TABLE 2

Total Fatty Acids (nmol/ml) in E. coli (*fadD*)

Strain	12:0	14:0	14:1	16:0	16:1	18:1
Control	3	19	2	141	59	42
MYRF-1	19	277	19	121	299	54
MYRF-2	32	240	31	47	296	17
CINC-1	99	195	204	43	102	26
CUPH-4	3	217	0	277	107	112

In comparison to the control, 14:0 and 16:1 fatty acids are drastically elevated for the nutmeg, camphor and *C. hookeriana* clones. Increases in 12:0 and 14:1 are also observed with the nutmeg and camphor clones, and increases in

16:0 and 18:1 are also seen with the *C. hookeriana* CUPH-4 clone.

E. Assay for Thioesterase Activity

For thioesterase activity assays, *E. coli* cells containing the acyl-ACP thioesterase constructs, and a similar culture of control cells are grown at 30°C to an OD_{600} of ~0.5. Induction of thioesterase expression in *lacZ* fusion constructs may be achieved by the addition of IPTG to 0.4 mM followed by 1 or 2 hours further growth. For slow growing cultures, longer growth periods may be required following addition of IPTG.

A ten-ml aliquot of each culture (containing cells plus the culture medium) is assayed for specific activity towards various carbon chain length acyl-ACP substrates as follows. Cells are harvested by centrifugation, resuspended in 0.5 ml assay buffer and lysed by sonication. Cell debris may be removed by further centrifugation. The supernatant is then used in thioesterase activity assays as per Pollard *et al.*, *Arch. Biochem & Biophys.* (1991) *281*:306-312. Results of thioesterase activity assays on *Cuphea*, nutmeg and camphor thioesterase clones using 8:0, 10:0, 12:0, 14:0, 16:0, 18:0 and 18:1 acyl-ACP substrates are provided in Table 3 below. Results are presented as relative activity of the thioesterase expressing cells compared to control cells.

TABLE 3

Relative Activity (TE/Control)

Strain	8:0	10:0	12:0	14:0	16:0	18:0	18:1
MCT34HT	0.9	0.8	1.0	42.8	21.8	1.5	
MYRF-1	1.1	1.4	1.8	13.6	13.3	5.5	13.6
MYRF-2	0.9	0.9	0.8	4.2	6.6	2.8	10.9
CINC-1		1.3	1.9	8.9	2.0	1.1	1.1

Substantial increases in the hydrolysis activity on 14:0 and 16:0 relative to the control cells are observed with *C. palustris* MCT34HT transformed cells. Cells transformed with the nutmeg MYRF-1 and MYRF-2 clones also demonstrate substantial increases in activity on 14:0 and 16:0 substrates,

as well as less substantial increases with 18:0 and 18:1. Expression of the camphor CINC-1 clone results mainly in increased activity on 14:0, although a lesser increase in 16:0 hydrolysis activity is also observed.

Example 3 - Constructs for Plant Transformation

A. Napin Expression Cassette

A napin expression cassette, pCGN1808, is described in copending US Patent Application serial number 07/742,834 which is incorporated herein by reference. pCGN1808 is modified to contain flanking restriction sites to allow movement of only the expression sequences and not the antibiotic resistance marker to binary vectors. Synthetic oligonucleotides containing *Kpn*I, *Not*I and *Hin*dIII restriction sites are annealed and ligated at the unique *Hin*dIII site of pCGN1808, such that only one *Hin*dIII site is recovered. The resulting plasmid, pCGN3200 contains unique *Hin*dIII, *Not*I and *Kpn*I restriction sites at the 3'-end of the napin 3'-regulatory sequences as confirmed by sequence analysis.

The majority of the napin expression cassette is subcloned from pCGN3200 by digestion with *Hin*dIII and *Sac*I and ligation to *Hin*dIII and *Sac*I digested pIC19R (Marsh, *et al.* (1984) *Gene 32*:481-485) to make pCGN3212. The extreme 5'-sequences of the napin promoter region are reconstructed by PCR using pCGN3200 as a template and two primers flanking the *Sac*I site and the junction of the napin 5'-promoter and the pUC backbone of pCGN3200 from the pCGN1808 construct. The forward primer contains *Cla*I, *Hin*dIII, *Not*I, and *Kpn*I restriction sites as well as nucleotides 408-423 of the napin 5'-sequence (from the EcoRV site) and the reverse primer contains the complement to napin sequences 718-739 which include the unique *Sac*I site in the 5'-promoter. The PCR was performed using in a Perkin Elmer/Cetus thermocycler according to manufacturer's specifications. The PCR fragment is subcloned as a blunt-ended fragment into pUC8 (Vieira and Messing (1982) *Gene 19*:259-268) digested with *Hinc*II to give pCGN3217. Sequenced of pCGN3217 across the napin insert verifies that no improper nucleotides were introduced by PCR. The napin 5-sequences in pCGN3217 are ligated to the remainder of the napin expression cassette by

digestion with *Cla*I and *Sac*I and ligation to pCGN3212 digested with *Cla*I and *Sac*I. The resulting expression cassette pCGN3221, is digested with *Hin*dIII and the napin expression sequences are gel purified away and ligated to pIC20H (Marsh, *supra*) digested with *Hin*dIII. The final expression cassette is pCGN3223, which contains in an ampicillin resistant background, essentially identical 1.725 napin 5' and 1.265 3' regulatory sequences as found in pCGN1808. The regulatory regions are flanked with *Hin*dIII, *Not*I and *Kpn*I restriction sites and unique *Sal*I, *Bgl*II, *Pst*I, and *Xho*I cloning sites are located between the 5' and 3' noncoding regions.

B. Oleosin Expression Cassette

A cassette for cloning of sequences for transcription under the regulation of 5' and 3' regions from an oleosin gene may be prepared. Sequence of a *Brassica napus* oleosin gene is provided by Lee and Huang (*Plant Phys.* (1991) *96*:1395-1397). Primers to the published sequence are used in PCR reactions to obtain the 5' and 3' regulatory regions of an oleosin gene from *Brassica napus* cv. Westar. Two PCR reactions were performed, one to amplify approximately 950 nucleotides immediately upstream of the ATG start codon for the oleosin gene, and one to PCR amplify approximately 600 bp including and downstream of the TAA stop codon for the oleosin gene. The PCR products were cloned into plasmid vector pAMP1 (BRL) according to manufacturer's protocols to yield plasmids pCGN7629 which contains the oleosin 5' flanking region and pCGN7630 which contains the 3' flanking region. The PCR primers included convenient restriction sites for cloning the 5' and 3' flanking regions together into an expression cassette. A *Pst*I fragment containing the 5' flanking region from pCGN7629 was cloned into *Pst*I digested pCGN7630 to yield plasmid pCGN7634. The *Bss*HII (New England BioLabs) fragment from pCGN7634, which contains the entire oleosin expression cassette was cloned into *Bss*HII digested pBCSK+ (Stratagene) to provide the oleosin cassette in a plasmid, pCGN7636. Sequence of the oleosin cassette in pCGN7636 is provided in Figure 7. The oleosin cassette is flanked by *Bss*HII, *Kpn*I and *Xba*I restriction sites, and contains *Sal*I, *Bam*HI and *Pst*I sites for insertion of wax

synthase, reductase, or other DNA sequences of interest between the 5' and 3' oleosin regions.

C. *C. palustris* Acyl-ACP Thio sterase Expression Constructs

Constructs for expression of *C. palustris* thioesterase cDNA clone MCT34 in plant seeds under the regulatory control of napin and oleosin regulatory regions are prepared as follows. The thioesterase encoding region from MCT34 is obtained by PCR amplification using oligonucleotides for insertion of a *SalI* site 5' to the ATG start codon, and an *NsiI* site immediately 3' to the MCT34 translation stop codon. The oligonucleotide primers for PCR contained the *SalI* site (CpMet-1 forward primer) and the *NsiI* site (CpStop-1 reverse primer). In addition, the primers contain "CAU" (forward primer) and "CUA" (reverse primer) repeat sequences for cloning using the CLONEAMP™ system. Sequence of the PCR primers is as follows:

CpMet-1 5' CAUCAUCAUCAUGTCGACAAACATGGTGGCTGCCGCAG 3'
CpStop-1 5' CUACUACUACUAATGCATTACTAAGATATAGAGTTTCCATTTG 3'.

The resulting PCR product is cloned into pAMP and the DNA sequence determined to verify the PCR products.

The *C. palustris* thioesterase pAMP clone (pCGN3860) is digested with *SalI* and *NsiI* and the thioesterase encoding fragment isolated and cloned into *SalI*/*PstI* digested pCGN3223 (napin expression cassette) or pCGN7636 (oleosin expression cassette), resulting in pCGN3861 and pCGN3862, respectively.

Binary vectors for plant transformation with the *C. palustris* expression constructs are prepared by digestion of pCGN3861 and pCGN3862 with *Asp*718 and insertion of the resulting fragments into *Asp*718 digested pCGN1578 (McBride *et al.* (1990) *Plant Mol. Biol. 14*:269-276), resulting in pCGN3863 and pCGN3864, respectively.

D. Nutmeg Acyl-ACP Thioesterase Expression Construct

Constructs for expression of nutmeg thioesterase cDNA clone MfFatB1 (pCGN3856 or MYRF-2) in plant seeds under the regulatory control of napin and oleosin regulatory regions are prepared as follows. The thioesterase encoding region from MfFatB1 is obtained by PCR amplification using oligonucleotides for insertion of a *BamHI* site 5' to the ATG start codon, and an

*Xho*I site 3' to the MfFatB1 translation stop codon. The oligonucleotide primers for PCR contained the *Bam*HI site (forward or sense primer) and the *Xho*I site (reverse or antisense primer). In addition, the primers contain "CAU" (forward primer) and "CUA" (reverse primer) repeat sequences for cloning using the CLONEAMP™ system. Sequence of the PCR primers is as follows:

Sense 5' CAUCAUCAUCAUGGATCCCTCATCATGGTTGCCACATCTGC 3'
Antisense 5' CUACUACUACUACTCGAGTTACATTTTGGCTATGC 3'.

The resulting PCR product is cloned into pAMP and the DNA sequence determined to verify the PCR products.

The nutmeg thioesterase pAMP clone (TA431) is digested with *Xho*I and partially digested with *Bam*HI. The thioesterase encoding fragment is isolated (1.3kb band) and cloned into *Bgl*II/*Xho* digested pCGN3223 (napin expression cassette), resulting in pCGN3868. A binary vector for plant transformation with the nutmeg expression construct is prepared by digestion of pCGN3868 with *Asp*718, and insertion of the resulting napin 5'/nutmeg TE/ napin 3'fragment (4.2kb) into pCGN1578PASS at the *Asp*718 site. [pCGN1578PASS is prepared from pCGN1578 (McBride *et al., supra*) by substitution of the pCGN1578 polylinker region with a polylinker region containing the following restriction sites: *Asp*718, *Asc*, *Pac*, *Swa*, *Sse* and *Hin*dIII.] The resulting construct, pCGN3854, is used for plant transformation for production of C14 fatty acids.

A construct for expression of the nutmeg thioesterase under the regulatory control of an oleosin promoter is prepared as follows. pCGN3868 (napin 5'/nutmeg TE/napin 3' expression construct described above) is digested with *Sal*I and *Eco*RV, and the resulting fragment, containing the nutmeg thioesterase encoding region joined in the 5' to 3' orientation to the napin 3' regulatory region, is inserted into *Sal*I and *Eco*RV digested pCGN7636 (oleosin expression cassette described above). The resulting construct, pCGN3858, contains an oleosin 5'/nutmeg TE/ napin 3'/oleosin 3' construct. pCGN3858 is digested with *Asp*718 and partially digested with *Bam*HI to produce an ~2.6kb fragment containing the oleosin 5', nutmeg thioesterase

encoding region, and ~320 nucleotides of the napin 3' regulatory region. The 2.6kb fragment is cloned into *Asp*718/*Bam*HI digested pCGN1578, resulting in pCGN3857, a binary vector for plant transformation and expression of the nutmeg thioesterase.

E. Camphor Acyl-ACP Thioesterase Expression Construct

A construct for expression of camphor thioesterase under the regulatory control of a napin promoter is described. A transit peptide encoding sequence for bay thioesterase is obtained by digestion of pCGN3826 (bay C12 preferring acyl-ACP thioesterase clone described in WO 92/20236) with *Xba*I and *Sal*I generating a DNA fragment having a plasmid vector backbone and the bay transit peptide encoding sequence (*Xba*I site is at beginning of mature bay protein encoding region). pCGN5220 (Example 2D) is digested with *Xba*I and *Sal*I to obtain the camphor mature TE encoding region. The pCGN5220 and pCGN3826 *Sal*I/*Xba*I fragments are ligated to produce pCGN5231. pCGN5231 is digested with *Bam*HI and *Sal*I, and the resulting bay transit::camphor mature encoding fragment is inserted into *Bgl*II/*Xho*I digested pCGN3223 (napin expression cassette), resulting in pCGN5232. pCGN5232 was digested with *Not*I and, with Klenow to produce blunt ends, and the resulting napin 5'/bay transit::camphor mature/napin 3' fragment is inserted into *Hin*dIII digested and Klenow-blunted pCGN1578. The resulting construct, pCGN5233, is a binary vector for plant transformation and expression of camphor thioesterase.

Example 4 Plant Transformation

A. *Brassica* Transformation

Brassica species may be transformed as reported by Radke *et al.* (*Plant Cell Reports* (1992) *11*:499-505; *Theor. Appl. Genet.* (1988) *75*:685-694), or as described in detail below.

Brassica napus seeds are soaked in 95% ethanol for 2 min. surface sterilized in a 1.0% solution of sodium hypochlorite containing a drop of Tween 20 for 45 min., and rinsed three times in sterile, distilled water. Seeds are then plated in Magenta box s with 1/10th concentration of Murashige minimal organics medium (Gibco; Grand Island,NY) supplemented with pyriodoxine (50µg/l), nicotinic acid (50µg/l), glycine

(200µg/l), and 0.6% Phytagar (Gibco) pH 5.8. Seeds are germinated in a Percival chamber at 22°C. in a 16 h photoperiod with cool fluorescent and red light of intensity approximately 65µ Einsteins per square meter per second ($\mu Em^{-2}s^{-1}$).

Hypocotyls are excised from 5-7 day old seedlings, cut into pieces approximately 4mm in length, and plated on feeder plates (Horsch *et al.*, *Science* (1985) *227*:1229-1231). Feeder plates are prepared one day before use by plating 1.0ml of a tobacco suspension culture onto a petri plate (100x25mm) containing about 30ml MS salt base (Carolina Biological, Burlington, NC) 100mg/l inositol, 1.3mg/l thiamine-HCl, 200mg KH_2PO_4 with 3% sucrose, 2,4-D (1.0mg/l), 0.6% w/v Phytagar, and pH adjusted to 5.8 prior to autoclaving (MS 0/1/0 medium). A sterile filter paper disc (Whatman 3mm) is placed on top of the feeder layer prior to use. Tobacco suspension cultures are subcultured weekly by transfer of 10ml of culture into 100ml fresh MS medium as described for the feeder plates with 2,4-D (0.2mg/l), Kinetin (0.1mg/l). In experiments where feeder cells are not used hypocotyl explants are cut and placed onto a filter paper disc on top of MS0/1/0 medium. All hypocotyl explants are preincubated on feeder plates for 24 h. at 22°C in continuous light of intensity $30\mu Em^{-2}s^{-1}$ to $65\mu EM^{-2}s^{-1}$.

Single colonies of *A. tumefaciens* strain EHA 101 containing a binary plasmid are transferred to 5ml MG/L broth and grown overnight at 30°C. Hypocotyl explants are immersed in 7-12ml MG/L broth with bacteria diluted to $1x10^8$ bacteria/ml and after 10-25 min. are placed onto feeder plates. Per liter MG/L broth contains 5g mannitol, 1g L-Glutamic acid or 1.15g sodium glutamate, 0.25g kH_2PO_4, 0.10g NaCl, 0.10g $MGSO_4 \cdot 7H_20$, 1mg biotin, 5g tryptone, and 2.5g yeast extract, and the broth is adjusted to pH 7.0. After 48 hours of co-incubation with *Agrobacterium*, the hypocotyl explants are transferred to B5 0/1/0 callus induction medium which contains filter sterilized carbenicillin (500mg/l, added after autoclaving) and kanamycin sulfate (Boehringer Mannheim; Indianapolis, IN) at concentrations of 25mg/l.

After 3-7 days in culture at $65\mu EM^{-2}s^{-1}$ continuous light, callus tissue is visible on the cut surface and the hypocotyl explants are transferred to shoot induction medium, B5BZ (B5

salts and vitamins supplemented with 3mg/l benzylaminopurine, 1mg/l zeatin, 1% sucrose, 0.6% Phytagar and pH adjusted to 5.8). This medium also contains carbenicillin (500mg/l) and kanamycin sulfate (25mg/l). Hypocotyl explants are subcultured onto fresh shoot induction medium every two weeks.

Shoots regenerate from the hypocotyl calli after one to three months. Green shoots at least 1cm tall are excised from the calli and placed on medium containing B5 salts and vitamins, 1% sucrose, carbenicillin (300mg/l), kanamycin sulfate (50mg/l) and 0.6% w/v Phytagar). After 2-4 weeks shoots which remain green are cut at the base and transferred to Magenta boxes containing root induction medium (B5 salts and vitamins, 1% sucrose, 2mg/l indolebutyric acid, 50mg/l kanamycin sulfate and 0.6% Phytagar). Green rooted shoots are tested for thioesterase activity.

B. *Arabidposis* Transformation

Transgenic *Arabidopsis thaliana* plants may be obtained by *Agrobacterium*-mediated transformation as described by Valverkens *et al.*, (*Proc. Nat. Acad. Sci.* (1988) *85*:5536-5540). Constructs are transformed into *Agrobacterium* cells, such as of strain EHA101 (Hood *et al.*, *J. Bacteriol* (1986) *168*:1291-1301), by the method of Holsters *et al.* (*Mol. Gen. Genet.* (1978) *163*:181-187).

C. Peanut Transformation

DNA sequences of interest may be introduced as expression cassettes, comprising at least a promoter region, a gene of interest, and a termination region, into a plant genome via particle bombardment as described in European Patent Application 332 855 and in co-pending application USSN 07/225,332, filed July 27, 1988.

Briefly, tungsten or gold particles of a size ranging from 0.5μM-3μM are coated with DNA of an expression cassette. This DNA may be in the form of an aqueous mixture or a dry DNA/particle precipitate.

Tissue used as the target for bombardment may be from cotyledonary explants, shoot meristems, immature leaflets, or anthers.

The bombardment of the tissue with the DNA-coated particles is carried out using a Biolistics™ particle gun

(Dupont; Wilmington, DE). The particles are placed in the barrel at variable distances ranging from 1cm-14cm from the barrel mouth. The tissue to be bombarded is placed beneath the stopping plate; testing is performed on the tissue at distances up to 20cm. At the moment of discharge, the tissue is protected by a nylon net or a combination of nylon nets with mesh ranging from 10μM to 300μM.

Following bombardment, plants may be regenerated following the method of Atreya, *et al.*, (*Plant Science Letters* (1984) *34*:379-383). Briefly, embryo axis tissue or cotyledon segments are placed on MS medium (Murashige and Skoog, *Physio. Plant.* (1962) *15*:473) (MS plus 2.0 mg/l 6-benzyladenine (BA) for the cotyledon segments) and incubated in the dark for 1 week at 25 ± 2°C and are subsequently transferred to continuous cool white fluorescent light (6.8 W/m^2). On the 10th day of culture, the plantlets are transferred to pots containing sterile soil, are kept in the shade for 3-5 days are and finally moved to greenhouse.

The putative transgenic shoots are rooted. Integration of exogenous DNA into the plant genome may be confirmed by various methods know to those skilled in the art.

Example 5 - Analysis of Transgenic Plants

A. Nutmeg (MYRF-2) Expression Construct

Mature seeds were harvested from transgenic *Brassica napus* plants (a QL01 derived low linolenic variety) containing pCGN3854, a construct for expression of nutmeg thioesterase clone MYRF-2 under the regulatory control of a napin promoter, and analyzed to determine mole percent fatty acid composition. Results are presented in Table 4 below.

TABLE 4

Plant	8:0	10:0	12:0	14:0	16:0	16:1	18:0	18:1	18:2	18:3
3854-1	0.00	0.26	0.30	13.50	22.10	0.49	4.84	37.62	16.26	1.96
3854-2	0.00	0.42	0.26	14.91	29.05	0.52	6.87	25.76	17.73	1.70
3854-3	0.00	0.27	0.43	21.73	30.90	0.43	6.48	19.54	15.85	1.62
3854-4	0.00	0.33	0.28	15.24	26.89	0.51	6.28	29.61	16.33	1.84

C14 fatty acyl groups are present in all four transgenic plants analyzed, with levels of C14 ranging from 13.5 to 21.73 mole perc nt. An even greater increase in C16 levels is observed, with ratios of C16 to C14 fatty acids ranging up to approximately 2:1. Generally, the C16/C14 ratio decreases with increasing C14 content, with ratios as low as approximately 1.3:1 being observed. A graph of the C14 and C16 levels in these transgenic plant seeds is provided in Figure 11. Background levels of C14 in non-transformed control plants are approximately 0.1 mole percent. Levels of C16 in non-transformed seeds of QL01 are approximately 4 mole percent. Single seeds from transformant 3854-3 are disected for half seed lipid analysis. Results from these analyses are presented in Table 5 below.

TABLE 5

NO.	8:0	10:0	12:0	14:0	16:0	16:1	18:0	18:1	18:2	18:3
1	0.00	2.31	0.40	19.11	29.78	0.36	6.63	22.69	14.08	1.46
2	0.00	1.84	0.37	20.26	30.45	0.44	5.76	19.30	17.49	1.51
3	0.00	1.53	0.37	16.87	29.24	0.49	8.11	25.66	13.06	1.44
4	0.00	2.39	0.44	20.82	29.96	0.58	6.02	18.47	16.78	1.68
5	0.00	2.91	0.43	19.66	30.16	0.62	6.71	23.12	12.43	1.48
6	0.00	2.01	0.40	18.52	29.50	0.36	6.99	23.49	14.01	1.67
7	0.00	4.02	0.51	23.04	29.94	0.25	5.30	17.16	16.13	1.75
8	0.00	3.13	0.38	18.03	27.87	0.58	6.09	25.51	14.31	1.51
9	0.00	3.00	0.44	21.23	29.19	0.63	5.68	17.58	18.34	1.85
12	0.00	2.52	0.34	17.80	28.93	0.38	6.73	23.62	15.11	1.53
13	0.00	2.56	0.45	21.48	30.59	0.49	6.02	18.43	16.02	1.48
14	0.00	2.19	0.39	18.40	30.48	0.47	7.44	23.39	12.68	1.42
15	0.00	1.88	0.28	15.17	28.81	0.44	7.73	28.03	12.94	1.35
16	0.00	2.10	0.38	19.83	30.34	0.43	6.23	20.33	15.95	1.33
17	0.00	2.44	0.42	18.73	28.89	0.60	7.21	22.26	14.83	1.68
18	0.00	2.77	0.45	20.32	29.55	0.47	6.55	21.93	13.93	1.46
19	0.00	3.37	0.40	17.72	27.95	0.48	6.38	24.22	14.01	2.01
20	0.00	2.40	0.36	19.72	29.92	0.50	6.72	19.79	16.10	1.52

Additional single seed fatty acid composition data (mole percent fatty acids) from 3854-3 and 3854-11 are presented in Figure 8. These data indicate C14 levels of up to 23% and C16 levels of up to 38% are obtained by expression of nutmeg thioesterase. In addition, smaller increases in 18:0 fatty acid levels are observed, with levels increasing from 1 mole

percent in non-transformed se ds of QL01 to levels of up to 9 mole percent in the transgenic seeds. Total saturated fatty acid lev ls in the transgenic seeds range from approximately 55 to 60 mole percent.

B. Camphor Expression Construct

Mature seeds were harvested from transgenic *Brassica napus* plants containing pCGN5233, a construct for expression of camphor thioesterase clone CINC-1 under the regulatory control of a napin promoter, and analyzed to determine mole percent fatty acid composition. Results are presented in Table 6 below.

TABLE 6

Plant	8:0	10:0	12:0	14:0	16:0	16:1	18:0	18:1	18:2	18:3
5233-1	0.00	0.84	0.87	6.93	9.64	0.95	1.51	41.35	21.47	14.99
5233-2	0.00	0.85	0.38	3.83	8.41	0.70	1.43	46.33	21.71	14.98
5233-4	0.00	0.96	1.33	11.46	11.69	1.06	1.16	31.07	23.54	16.26
5233-5	0.00	0.69	0.93	8.77	10.38	0.90	1.48	42.22	19.88	13.41
5233-6	0.00	0.69	1.29	11.38	10.98	0.83	1.54	40.75	18.32	12.98
5233-7	0.00	0.70	0.36	4.44	8.57	0.73	1.22	45.26	21.29	16.06
5233-8	0.00	1.07	0.24	2.46	7.67	0.85	1.25	47.47	22.51	14.90
5233-9	0.00	0.94	0.58	5.37	9.06	0.68	1.42	46.70	20.26	13.95
5233-10	0.00	0.83	0.26	2.84	7.89	0.74	1.26	46.21	21.68	16.88
5233-11	0.00	1.06	0.19	1.78	7.43	0.69	1.16	49.30	21.79	15.07
5233-12	0.00	0.69	0.51	5.42	9.02	0.77	1.40	46.09	19.81	15.03
5233-13	0.00	0.65	0.04	0.11	5.49	0.46	1.25	51.21	22.32	16.82
5233-14	0.00	0.81	0.64	6.46	9.54	0.86	1.21	44.11	20.50	14.33
5233-15	0.00	0.88	0.24	2.79	8.16	0.72	1.40	47.47	21.50	15.35
5233-16	0.00	1.00	0.35	3.52	8.03	0.66	1.35	44.98	23.01	15.94
5233-17	0.00	0.86	0.78	7.89	10.63	1.01	1.37	42.11	20.58	13.17
5233-18	0.00	1.53	0.62	6.25	10.14	0.83	1.37	39.80	23.38	15.64
5233-19	0.00	1.29	0.27	2.43	8.46	1.19	1.72	45.19	23.78	13.60
5233-20	0.00	1.23	0.34	3.59	9.49	1.03	1.87	48.74	19.24	12.93
5233-21	0.00	0.82	0.23	1.97	7.27	0.77	1.26	49.20	22.11	14.91
5233-22	0.00	0.60	0.54	5.63	9.64	0.75	1.56	45.07	21.94	12.53
5233-24	0.00	0.77	0.54	6.08	9.67	0.84	1.27	42.47	21.15	15.74
Control	0.00	0.74	0.02	0.10	6.15	0.66	1.48	51.75	21.03	16.22

An increased percentage of C14 fatty acyl groups above control plant background levels is observed in all but one of the transgenic plants analyzed. The levels of C14 range from approximately 2.0 mole percent to 11.5 mole percent.

Single seed data from transformants 5233-5 and 5233-6 are presented in Figure 9. These results demonstrate C14 levels of greater than 20% are obtained in seeds expressing a camphor FatB thioesterase. Increases in 16:0 levels from approximately 6 mole % in seeds from non-transformed control plants up to approximately 15 mole % are obtained. To a lesser extent, increases in 12:0 fatty acyl groups are also observed.

At lower levels of C14, the C16 levels may be up to 2-3 times that of the C14 levels. At higher C14 levels, the C16 levels are equal to or less than the C14 levels. A graph of the C14 and C16 levels in these transgenic plant seeds is provided in Figure 11. Total saturated fatty acid contents of up to 40 mole % are detected in these seeds.

C. *C. palustris* Expression Construct

Analysis of pooled seeds from 3863-transformants reveals C14 levels of up to approximately 37 mole percent. Data from analysis of fatty acid compositions of single seeds from transformants 3863-10, 3863-7, 3863-4, 3863-8, 3863-2, and 3863-5 are presented in Figure 10. These data indicate C14 levels of greater than 40% are obtained by expression of *C. palustris* FatB2 thioesterase clone. C14 levels exceed C16 levels at a ratio of approximately 2:1 in most of the 3863 transformant seeds. However, when C14 levels are low (less than approximately 15%), C16 levels are generally higher than C14 levels. A graph of the C14 and C16 levels in the nutmeg, *C. palustris* and camphor TE transgenic plant seeds is provided in Figure 11.

D. Oleosin Promoter/C14 Thioesterase Constructs

Analysis (mole percent fatty acids) of pooled seed samples from *B. napus* transgenic plants expressing the *C. palustris* (3864) or the nutmeg (3857) C14 thioesterases is provided in Figure 12. As with napin promoter constructs, expression of nutmeg thioesterase results in increased production of C14 and C16 fatty acids at a ratio of approximately 2:1 C16/C14 fatty acids. With expression of *C. palustris* C14 thioesterase, C14 is generally produced in greater amounts than C16 as was observed with napin/*C. palustris* C14 thioesterase constructs. Generally, levels of C14 and C16 fatty acids obtained by expression of thioesterases under regulatory control of the

oleosin promoter are lower than the levels obtained by expression using th napin promoter.

E. C14 thioesterase and Medium-chain LPAAT Expressing Plants

Napin/*C. palusatris* transformant 3863-6, seeds of which comprise approximately 20 mole percent 14:0 and 13 mole percent 16:0, is crossed with a *B. napus* transformant comprising a coconut medium-chain preferring LPAAT expression construct, pCGN5511. (See WO 95/27791.) Fatty acyl composition analysis of segregating pooled seeds from the resulting F1 plants reveal average levels of 10 mole percent 14:0 and 7 mole percent 16:0. Fatty acyl composition at the *sn*-2 position are determined for pooled segregating seed samples from the 3863-6 plants and the F1 plants resulting from the 5511 X 3863-6 cross.

For *sn*-2 analysis oil distilled from mature seeds is subjected to a lipase digestion protocol modified from Brockerhoff *et al.* (*Meth. Enzymol.* (1975) *35*:315-325)), to minimize acyl migration. This distinguishes acyl compositions of the sn-2 and sn-1+3 combined positions. The modifications are briefly as follows: pH is lowered to neutrality, reaction time is shortened, samples are maintained at acidic pH thereafter, and digestion products are chromatographed on borate-impregnated TLC plants. The chromatographed products are then eluted and analyzed as fatty acid methyl esters as before. In this manner the percentage of fatty acids, such as medium-chain C12 or C14 fatty acids or long-chain C22:1 fatty acids in the *sn*-2 position is determined. The modified procedure was verified using steochemically defined structured TAGs and is conducted as follows.

Generally in the lipase procedure, only positive-displacement pipetors are used as oil and organic solvents cannot be delivered reliably by negative-displacement pipetors. Additionally, care should be taken when evaporating solvents to bring the sample only barely to dryness. When C10 or shorter acyl groups are present avoid dryness altogether. Plasticware or kitchen glassware that can contribute fatty acid contamination should be avoided. Glassware may be pre-rinsed with chloroform/methanol 2/1 (v/v) if necessary.

In 15-ml screw-cap (teflon liner) vial combine 2 ml 0.1M Tris-HCl, pH 7.0, 0.2 ml 2.2% w/v $CaCl_2$, 0.5 ml 0.05% w/v bile

salts (Sigma), and 10 µl (10 µg if solid) oil or TAG sample. Sonicate briefly in a sonication bath to disperse at least some of the oil. The suspension should develop a cloudy appearance after a few minutes.

Prepare lipase dilution using an active suspension of lipase, such as *Rhizopus arrhizus* lipase (Sigma, L4384) and hold on ice (4°C). (Activity will be lost if suspension is frozen). Enzyme batches may be checked by testing various dilutions of the suspension with water in the overall procedure, using oil containing unsaturated fatty acids and visualizing the extent of digestion by System 1 TLC (see below) with iodine staining. The correct dilution should result in approximately 50% digestion of the TAG. (Further digestion risks increasing attack on the MAG product.) Typically dilution of the Sigma *Rhizopus arrhizus* lipase suspension with water to about 600,000 units/ml gives an appropriate concentration.

Each reaction is run individually. Add 100 µl of the water-diluted lipase to start the reaction, cap the vial, and immediately start a continuous vortex mixing for 1.5 minutes. Make and break the vortex several times during this mixing so as to prevent stratification. A white ppt must form during the 1.5 min "incubation". The precipitate comprises calcium salts of released fatty acids, and is an indication that the reaction is proceeding.

At the end of the 1.5 min mixing incubation, stop the reaction by adding 0.5 ml 6M HCl and mixing briefly. Immediately add 2.6 ml chloroform/methanol 2/1 v/v, shake well and place in ice while the other lipase digestions are performed. Note that the white ppt will now completely redissolve.

Remove all the vials from ice, mix well once again, and spin briefly to sharpen the layers. The digestion products are in the lower layer. Using a Pasteur pipet remove the lower layer to a new 15-ml vial. Re-extract the original digestion mixture with 1.6 ml straight chloroform, mix well, spin, and combine this lower layer with the previously removed one. The combined lower, organic layers are blown to near-dryness under

N_2 and just enough heat to prevent the samples from getting very cold.

The TLC plates for acyl migration are 500 µm preparative Sil-G pre-loaded with boric acid and containing no fluorescent indicator. The pre-loading is carried out by ascending migration of 5% w/v boric acid in 1/1 v/v acetonitrile/methanol for at least 90 minutes. The plated are dried and stored at room temperature until ready for use. Heating "activation" may be necessary in damp climates.

Two solvent systems are suitable, both ascending the plates for exactly 1 hour even if the solvent doesn't reach the top of the plate, as longer runs result in reduced resolution due to the extreme volatility of the solvents.

System 1 - n-hexane/diethyl ether/acetic acid, 70/30/1 v/v
System 2 - Diethyl ether/acetic acid, 100/1 v/v

System 1 is used to evaluate and monitor the lipase reaction, as it allows recovery of TAG, DAG, fatty acid, and MAG. System 2 may be used for routine use and yields the best purity of the MAG product required for the *sn*-2 determination.

Prior to spotting the plates, score down the middle with a pencil so that two samples can be applied (left and right). (Sample chromatography is performed in the same direction as the borate loading.) Also remove 0.5 cm of layer from each side to eliminate edge effects, and draw a line 2 cm up from the bottom as a loading guide. Redissolve each dried sample in 100 µl chloroform/methanol 2/1 (v/v) and apply along the loading line on the half-plate. Rinse the vial twice with 100 µl chloroform/methanol 2/1 (v/v) each time and load over the top of the sample. Air-dry the loading area and run the solvent. Let plates air-dry in hood.

To ensure minimal acyl rearrangements for *sn*-1 and *sn*-3 analyses of the products, the procedure should be conducted without interruption from the start of the lipase reaction.

The TLC plates are visualized with Rhodamine spray, ~1% w/v Rhodamine 6G in acetone. The plates are sprayed until they are an overall medium-pink color, allowed to dry a few minutes, and viewed under UV light. Lipids fluoresce yellow on an

orange background. Desired zones are outlined in pencil. When using system 2, MAG zone is routinely 50-75% of the distance up the plat and the rest of the products are at the top. The MAG area may appear multi-zoned due to some chain-length resolution, but should be outlined for excision as a single overall zone.

The zones are scraped onto clean paper and transferred to large screw-cap (teflon liner) test tubes. Add 10 ml chloroform/methanol 2/1 (v/v), shake, and let stand for at least an hour. Filter through Whatman paper directly into 100-ml rotary evaporation flasks. Rinse the tubes twice through the filters with 5 ml chloroform/methanol 2/1 (v/v) each time. (The Rhodamine dye will co-elute with the lipids and will track with them through the procedure until the final hexane extraction of fatty acid methyl esters (FAMES), when it will be left behind.) Rotary-evaporate at room temperature or up to 30°C, to reduce volume to about 100 µl. Transfer to 15-ml screw-cap vial, along with a couple of 100 µl chloroform/methanol 2/1 (v/v) rinses of the flask, and blow down to near-dryness under N2.

To the nearly dry samples add 2 ml freshly-prepared 5% (w/v) sulfuric acid in methanol. Relatively new methanol which has not had a chance to absorb much water should be used. Also add to the samples 1 ml of toluene containing desired internal standard at 0.5 mg/ml TAG (*e.g.* tri-17:0 etc.). Incubate at 90°C for 2 hours, tightening the caps after the first 2 minutes and again after about 15 minutes. After the vials have cooled, add 2 ml 0.9% w/v NaCl and 0.5 ml n-hexane. Mix thoroughly, let stand a few minutess to separate layers, and sample the top layer into the g.c. vial. Fatty acid composition is determined by analysis for fatty acid methyl esters (FAME) as described by Browse *et al.* (*Anal. Biochem.* (1986) *152*:141-145).

The composition of the MAG zone is taken as the composition at *sn*-2 of the original oil or TAG sample. The average composition at the primary (*sn*-1 and -3) positions is computed using the formula (3TAG-MAG)/2 on the % of each acyl group.

The *sn*-2 analysis of T2 seed from 3863-6 reveals a 14:0 level of approximately 3 mole percent. Levels of 16:0 at the

sn-2 position were less than 1 mole percent. Analysis of *sn*-2 fatty acyl groups in F1 seeds from a 5511 X 3863-6 plant indicates 14:0 levels of approximately 9 mole percent. As with the 3863-6 plant seeds, the levels of 16:0 at the *sn*-2 position were less than 1 mole percent.

These data demonstrate that the expression of coconut medium-chain LPAAT in conjunction with expression of a plant C14 thioesterase provides for greater incorporation of myristate into the *sn*-2 position, effectively randomizing the distribution of 14:0, while the 16:0 distribution is unaffected. Thus, the combination of LPAAT and C14 thioesterase is especially desirable for overall increase in C14 fatty acids in transgenic plant seed oils.

The above results demonstrate the ability to obtain DNA sequences which encode thioesterase activities, which sequences may be expressed in plant seed cells for manipulation of seed oil fatty acid composition. In this manner production of significant levels of C14 fatty acids C14 may be obtained. The novel seed oils so produced may find uses in industry as whole oils, or can be fractionated using methods known in the industry to provide sources of the C14 fatty acids incorporated into the oil.

All publications and patent applications mentioned in this specification are indicative of the level of skill of those skilled in the art to which this invention pertains. All publications and patent applications are herein incorporated by reference to the same extent as if each individual publication or patent application was specifically and individually indicated to be incorporated by reference.

Although the foregoing invention has been described in some detail by way of illustration and example for purposes of clarity of understanding, it will be obvious that certain changes and modifications may be practiced within the scope of the appended claim.

What is claimed is:

1. A method of producing C14 fatty acids in plant seed triglycerides, wherein said method comprises:

growing a plant having integrated into its genome a DNA construct, said construct comprising in the 5' to 3' direction of transcription, a promoter functional in a plant seed cell, a DNA sequence encoding a protein having preferential hydrolysis activity on C14:0 acyl-ACP substrates as compared to other medium-chain acyl-ACP substrates, and a transcription termination region functional in a plant cell.

2. The method of Claim 1 wherein said plant is an oilseed crop plant.

3. The method of Claim 2 wherein said oilseed crop plant is a *Brassica* plant.

4. The method of Claim 1, wherein said protein is a plant acyl-ACP thioesterase.

5. The method of Claim 4 wherein said plant thioesterase encoding sequence is from *Cuphea*, nutmeg or camphor.

6. The method of Claim 4, wherein said plant acyl-ACP thioesterase has preferential activity on C14 acyl-ACP substrates.

7. The method of Claim 6, wherein said plant thioesterase encoding sequence is from *Cuphea palustris*.

8. The method of Claim 1, wherein said promoter is from a gene preferentially expressed in plant seed tissue.

9. The method of Claim 1, wherein said plant seed triglycerides comprise at least 5 mole percent C14 fatty acyl groups.

10. The method of Claim 1, wherein said plant seed triglycerides comprise at least 20 mole percent C14 fatty acyl groups.

11. The method of Claim 1, wherein said plant seed triglycerides comprise at least 40 mole percent C14 fatty acyl groups.

12. The method of Claim 1, wherein said plant seed triglycerides further comprise increased 16:0 fatty acyl content.

13. The method of Claim 12, wherein the level of 14:0 fatty acyl groups is greater than the level of 16:0 fatty acyl groups.

14. The method of Claim 12, wherein the level of 14:0 fatty acyl groups is less than the level of 16:0 fatty acyl groups.

15. A plant seed comprising a minimium of 5.0 mole percent myristate in total fatty acids, wherein said myristate is incorporated into at least one position of a triglyceride molecule and wherein wild-type seed of said plant contains less than 1.0 mole percent laurate in fatty acids.

16. The seed of Claim 15 comprising a minimum of about 20 mole percent myristate in fatty acids.

17. The seed of Claim 15 comprising a minimum of about 40 mole percent myristate in fatty acids.

18. Plant seed oil, wherein a minimium of 5.0 mole percent of the acyl groups of said oil are myristyl acyl groups, and wherein said oil is derived from a seed of Claim 15.

19. A *Brassica* seed comprising a minimum of 5.0 mole percent myristate in total fatty acids.

20. Plant seed oil, wherein a minimium of 5.0 mole percent of the acyl groups of said oil are myristyl acyl groups, and wherein said oil is derived from a *Brassica* seed of Claim 19.

21. A DNA construct comprising an encoding sequence for a plant acyl-ACP thioesterase having preferential activity on C14 acyl-ACP substrates as compared to other medium-chain acyl-ACP substrates.

22. A construct according to Claim 21 wherein said plant is a *Cuphea* species.

23. A construct according to Claim 22 wherein said species is *Cuphea palustris*.

24. A construct according to Claim 23 wherein said thioesterase comprises the amino acid sequence shown in Figure 1.

25. A construct according to Claim 22 wherein said plant is nutmeg.

26. A construct according to Claim 25 wherein said thioesterase comprises the amino acid sequence shown in Figure 2 or 3.

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GCTCTAATAC GACTCACTAT AGGGAAAGCT GGTACGCCTG CAGGTACCGG TCCGGAATTC    60

CCGGGTCGAC CCACGCGTCC GCTGAGTTTG CTGGTTACCA TTTTCCCTGC GAACAAAC     118

ATG GTG GCT GCC GCA GCA AGT GCT GCA TTC TTC TCC GTC GCA ACC CCG     166
Met Val Ala Ala Ala Ala Ser Ala Ala Phe Phe Ser Val Ala Thr Pro
 1               5                  10                  15

CGA ACA AAC ATT TCG CCA TCG AGC TTG AGC GTC CCC TTC AAG CCC AAA     214
Arg Thr Asn Ile Ser Pro Ser Ser Leu Ser Val Pro Phe Lys Pro Lys
            20                  25                  30

TCA AAC CAC AAT GGT GGC TTT CAG GTT AAG GCA AAC GCC AGT GCC CAT     262
Ser Asn His Asn Gly Gly Phe Gln Val Lys Ala Asn Ala Ser Ala His
        35                  40                  45

CCT AAG GCT AAC GGT TCT GCA GTA AGT CTA AAG TCT GGC AGC CTC GAG     310
Pro Lys Ala Asn Gly Ser Ala Val Ser Leu Lys Ser Gly Ser Leu Glu
    50                  55                  60

ACT CAG GAG GAC AAA ACT TCA TCG TCG TCC CCT CCT CCT CGG ACT TTC     358
Thr Gln Glu Asp Lys Thr Ser Ser Ser Ser Pro Pro Pro Arg Thr Phe
65                  70                  75                  80
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FIG.1A

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ATT AAC CAG TTG CCC GTC TGG AGT ATG CTT CTG TCT GCA GTC ACG ACT     406
Ile Asn Gln Leu Pro Val Trp Ser Met Leu Leu Ser Ala Val Thr Thr
                 85                  90                  95

GTC TTC GGG GTG GCT GAG AAG CAG TGG CCA ATG CTT GAC CGG AAA TCT     454
Val Phe Gly Val Ala Glu Lys Gln Trp Pro Met Leu Asp Arg Lys Ser
            100                 105                 110

AAG AGG CCC GAC ATG CTT GTG GAA CCG CTT GGG GTT GAC AGG ATT GTT     502
Lys Arg Pro Asp Met Leu Val Glu Pro Leu Gly Val Asp Arg Ile Val
        115                 120                 125

TAT GAT GGG GTT AGT TTC AGA CAG AGT TTT TCG ATT AGA TCT TAC GAA     550
Tyr Asp Gly Val Ser Phe Arg Gln Ser Phe Ser Ile Arg Ser Tyr Glu
    130                 135                 140

ATA GGC GCT GAT CGA ACA GCC TCG ATA GAG ACC CTG ATG AAC ATG TTC     598
Ile Gly Ala Asp Arg Thr Ala Ser Ile Glu Thr Leu Met Asn Met Phe
145                 150                 155                 160

CAG GAA ACA TCT CTT AAT CAT TGT AAG ATT ATC GGT CTT CTC AAT GAC     646
Gln Glu Thr Ser Leu Asn His Cys Lys Ile Ile Gly Leu Leu Asn Asp
                165                 170                 175
```

FIG.1B

```
GGC TTT GGT CGA ACT CCT GAG ATG TGT AAG AGG GAC CTC ATT TGG GTG      694
Gly Phe Gly Arg Thr Pro Glu Met Cys Lys Arg Asp Leu Ile Trp Val
            180                 185                 190

GTC ACG AAA ATG CAG ATC GAG GTG AAT CGC TAT CCT ACT TGG GGT GAT      742
Val Thr Lys Met Gln Ile Glu Val Asn Arg Tyr Pro Thr Trp Gly Asp
        195                 200                 205

ACT ATA GAG GTC AAT ACT TGG GTC TCA GCG TCG GGG AAA CAC GGT ATG      790
Thr Ile Glu Val Asn Thr Trp Val Ser Ala Ser Gly Lys His Gly Met
    210                 215                 220

GGT CGA GAT TGG CTG ATA AGT GAT TGC CAT ACA GGA GAA ATT CTT ATA      838
Gly Arg Asp Trp Leu Ile Ser Asp Cys His Thr Gly Glu Ile Leu Ile
225                 230                 235                 240

AGA GCA ACG AGC GTG TGG GCT ATG ATG AAT CAA AAG ACG AGA AGA TTG      886
Arg Ala Thr Ser Val Trp Ala Met Met Asn Gln Lys Thr Arg Arg Leu
                245                 250                 255

TCG AAA ATT CCA TAT GAG GTT CGA CAG GAG ATA GAG CCT CAG TTT GTG      934
Ser Lys Ile Pro Tyr Glu Val Arg Gln Glu Ile Glu Pro Gln Phe Val
            260                 265                 270
```

FIG.1C

```
GAC TCT GCT CCT GTC ATT GTA GAC GAT CGA AAA TTT CAC AAG CTT GAT      982
Asp Ser Ala Pro Val Ile Val Asp Asp Arg Lys Phe His Lys Leu Asp
        275                 280                 285

TTG AAG ACC GGT GAT TCC ATT TGC AAT GGT CTA ACT CCA AGG TGG ACT     1030
Leu Lys Thr Gly Asp Ser Ile Cys Asn Gly Leu Thr Pro Arg Trp Thr
    290                 295                 300

GAC TTG GAT GTC AAT CAG CAC GTT AAC AAT GTG AAA TAC ATC GGG TGG     1078
Asp Leu Asp Val Asn Gln His Val Asn Asn Val Lys Tyr Ile Gly Trp
305                 310                 315                 320

ATT CTC CAG AGT GTT CCC ACA GAA GTT TTC GAG ACG CAG GAG CTA TGT     1126
Ile Leu Gln Ser Val Pro Thr Glu Val Phe Glu Thr Gln Glu Leu Cys
                325                 330                 335

GGC CTC ACC CTT GAG TAT AGG CGA GAA TGC GGA AGG GAC AGT GTG CTG     1174
Gly Leu Thr Leu Glu Tyr Arg Arg Glu Cys Gly Arg Asp Ser Val Leu
            340                 345                 350

GAG TCC GTG ACC GCT ATG GAT CCA TCA AAA GAG GGA GAC CGG TCT CTT     1222
Glu Ser Val Thr Ala Met Asp Pro Ser Lys Glu Gly Asp Arg Ser Leu
        355                 360                 365
```

FIG.1D

```
TAC CAG CAC CTT CTC CGA CTC GAG GAC GGG GCT GAT ATC GTC AAG GGG    1270
Tyr Gln His Leu Leu Arg Leu Glu Asp Gly Ala Asp Ile Val Lys Gly
    370                 375                 380

AGA ACC GAG TGG CGG CCG AAG AAT GCA GGA GCC AAG GGA GCA ATA TTA    1318
Arg Thr Glu Trp Arg Pro Lys Asn Ala Gly Ala Lys Gly Ala Ile Leu
385                 390                 395                 400

ACC GGA AAG ACC TCA AAT GGA AAC TCT ATA TCT TAGAAGGAGG AAGGGACCTT 1371
Thr Gly Lys Thr Ser Asn Gly Asn Ser Ile Ser
                405                 410

TCCGAGTTGT GTGTTTATTT GCTTTGCTTT GATTCACTCC ATTGTATAAT AATACTACGG 1431

TCAGCCGTCT TTGTATTTGC TAAGACAAAT AGCACAGTCA TTAAGTTAAA AAAAAAAAAA 1491

AAGGGCGGCC GCTCTAGAGG ATCCAAGCTT ACGTACGCGT GCATGCGACG TCATAGCTCT 1551

TCTATAGTGT CACCTAAATT CAATTCACTG                                    1581
```

FIG.1E

```
CCG GAT TGG AGC ATG CTT CTT GCA GCA ATC ACA ACC ATC TTC TTG GCA      48
Pro Asp Trp Ser Met Leu Leu Ala Ala Ile Thr Thr Ile Phe Leu Ala
1               5                  10                  15

GCC GAG AAG CAG TGG ACG AAT CTT GAC TGG AAG CCC AGG AGG CCT GAC      96
Ala Glu Lys Gln Trp Thr Asn Leu Asp Trp Lys Pro Arg Arg Pro Asp
            20                  25                  30

ATG CTC GTC GAC TTT GAC CCT TTT AGT CTG GGG AGG TTC GTT CAG GAT     144
Met Leu Val Asp Phe Asp Pro Phe Ser Leu Gly Arg Phe Val Gln Asp
        35                  40                  45

GGG TTG ATT TTC AGG CAG AAT TTC TCC ATC AGG TCT TAT GAG ATT GGC     192
Gly Leu Ile Phe Arg Gln Asn Phe Ser Ile Arg Ser Tyr Glu Ile Gly
    50                  55                  60

GCG GAT CGG ACG GCA TCC ATA GAG ACG TTA ATG AAT CAT CTA CAG GAA     240
Ala Asp Arg Thr Ala Ser Ile Glu Thr Leu Met Asn His Leu Gln Glu
65                  70                  75                  80

ACG GCC CTA AAC CAT GTA AGG TGT ATA GGG CTC CTC GAT GAT GGT TTT     288
Thr Ala Leu Asn His Val Arg Cys Ile Gly Leu Leu Asp Asp Gly Phe
                85                  90                  95
```

FIG.2A

```
GGT TCG ACG CCT GAG ATG ACT AGG AGA GAT CTG ATA TGG GTG GTT ACA     336
Gly Ser Thr Pro Glu Met Thr Arg Arg Asp Leu Ile Trp Val Val Thr
            100                 105                 110

AGG ATG CAG GTT CTG GTG GAT CGC TAT CCT TCC TGG GGG GAT GTC ATT     384
Arg Met Gln Val Leu Val Asp Arg Tyr Pro Ser Trp Gly Asp Val Ile
        115                 120                 125

GAA GTA GAC TCC TGG GTT ACT CCA TCT GGA AAG AAT GGG ATG AAA CGT     432
Glu Val Asp Ser Trp Val Thr Pro Ser Gly Lys Asn Gly Met Lys Arg
    130                 135                 140

GAA TGG TTT CTC CGT GAT TGC AAG ACA GGC GAA ATC CTG ACA CGA GCT     480
Glu Trp Phe Leu Arg Asp Cys Lys Thr Gly Glu Ile Leu Thr Arg Ala
145                 150                 155                 160

ACC AGT GTT TGG GTG ATG ATG AAT AAA CGG ACA CGG AGG TTG TCC AAA     528
Thr Ser Val Trp Val Met Met Asn Lys Arg Thr Arg Arg Leu Ser Lys
                165                 170                 175

ATC CCT GAA GAA GTT AGA GTC GAA ATA GAG CCT TAT TTT GTG GAG CAT     576
Ile Pro Glu Glu Val Arg Val Glu Ile Glu Pro Tyr Phe Val Glu His
            180                 185                 190
```

FIG.2B

```
GGA GTC TTG GAT GAG GAC AGC AGA AAA CTA CCA AAG CTC AAT GAC AAC      624
Gly Val Leu Asp Glu Asp Ser Arg Lys Leu Pro Lys Leu Asn Asp Asn
        195                 200                 205

ACT GCA AAT TAC ATC AGA AGA GGC CTA GCT CCT CGG TGG AGT GAT TTA      672
Thr Ala Asn Tyr Ile Arg Arg Gly Leu Ala Pro Arg Trp Ser Asp Leu
    210                 215                 220

GAT GTC AAT CAG CAT GTG AAC AAT GTC AAA TAC ATT GGC TGG ATT CTT      720
Asp Val Asn Gln His Val Asn Asn Val Lys Tyr Ile Gly Trp Ile Leu
225                 230                 235                 240

GAG AGC GTG CCA TCT TCA CTG TTG GAG AGT CAT GAG CTG TAT GGG ATG      768
Glu Ser Val Pro Ser Ser Leu Leu Glu Ser His Glu Leu Tyr Gly Met
                245                 250                 255

ACA CTT GAG TAT AGG AAG GAG TGT GGA AAG GAC GGT TTG CTG CAA TCC      816
Thr Leu Glu Tyr Arg Lys Glu Cys Gly Lys Asp Gly Leu Leu Gln Ser
            260                 265                 270

CTG ACT GCT GTT GCC AGT GAT TAT GGG GGT GGA TCC CTT GAA GCT GGC      864
Leu Thr Ala Val Ala Ser Asp Tyr Gly Gly Gly Ser Leu Glu Ala Gly
        275                 280                 285
```

FIG.2C

```
GTT GAG TGT GAC CAC CTT CTT CGC CTT GAA GAT GGG AGT GAG ATT ATG     912
Val Glu Cys Asp His Leu Leu Arg Leu Glu Asp Gly Ser Glu Ile Met
    290                 295                 300

AGG GGA AAG ACG GAA TGG AGG CCC AAG CGT GCC GCC AAC ACT ACC TAC     960
Arg Gly Lys Thr Glu Trp Arg Pro Lys Arg Ala Ala Asn Thr Thr Tyr
305                 310                 315                 320

TTT GGA AGC GTT GAT GAT ATT CCT CCC CAC CCA ATA TAT ATA TAT ATA    1008
Phe Gly Ser Val Asp Asp Ile Pro Pro His Pro Ile Tyr Ile Tyr Ile
                325                 330                 335

TAT ATA TAT ATA TAT ATA TAT ATA TAT TGG GTG GGG AGC AGC TGC AGC    1056
Tyr Ile Tyr Ile Tyr Ile Tyr Ile Tyr Trp Val Gly Ser Ser Cys Ser
            340                 345                 350

GGC AGC AGC ACG ACA ATG TCG AGG ACA CGA TGACGATCAG TATGTTTCGT      1106
Gly Ser Ser Thr Thr Met Ser Arg Thr Arg
        355                 360

GCGGTATTTA GCAATTCCGT ATGTAGAATC CTGCGTGTAC TGGCAGATAA TTTTTTGATT 1166

TGTTCTTTTC GTTTACGAGG GGAACCCGTG TAATTAGTTC AACTGTATTT TCTGTTTCTT 1226
```

FIG.2D

```
CCTTAAGTGT TTCAACACCC CTCTCTCTCT CGCGCGCGCG CGTGCGCTCA CATTTTCCAT 1286

TCCTTTTCTT TTTATTCTAG TTGTACGAGT GGGAGTTCAT TTGCACTAAA TTGTTGAAAA 1346

ATCTCGTTGC TTGG                                                  1360
```

FIG.2E

```
GGAGAGCCGC CTCTTCAGCC CACCACCACC TCTAAAACAA CAGGCCCAAA ACTCCCTCCT    60

TTCTCTGTCC CTTTCCGGTG CTTCCCCCTC TATTTTAGAC CTCCTCCTTT ATATTTCCCA   120

ACGTAGAATA ATACCAAAAC CCTAAACCGA GAAGAAGATA AAAGAAAGAG GAGAGAGAAA   180

CAGAAAGAGA TAGAGAGAGA AAAAAAATCG GTCTTCTCTC TCTTTCTCTG TCGCTGCGAA   240

GGAGCGGCCG TGAAATTTGG TCATTTGCTA TGAGAAATAT TCCTTCTGTG ATGCTTGATT   300

TCTAATTTAA CGAGTCTGTA TCGTAATTTT CTCATC ATG GTT GCC ACA TCT GCT      354
                                       Met Val Ala Thr Ser Ala
                                       1               5

GCC TCC GCT TTC TTC CCG GTT GCC TCT CCG TCT CCA GTG AAG CCT TCG      402
Ala Ser Ala Phe Phe Pro Val Ala Ser Pro Ser Pro Val Lys Pro Ser
            10                  15                  20

ATG ATG CTC GGT GGT GGA GGA GGT TCG GAT AAT CTC GAC GCC CGT GGG      450
Met Met Leu Gly Gly Gly Gly Gly Ser Asp Asn Leu Asp Ala Arg Gly
        25                  30                  35

ATC AAA TCC CGC CCT GCC TCC TCT GGT GGC CTT CAA GTA AAG GCC AAT      498
Ile Lys Ser Arg Pro Ala Ser Ser Gly Gly Leu Gln Val Lys Ala Asn
    40                  45                  50
```

FIG.3A

```
GCT CAT ACT GTT CCC AAG ATC AAT GGT AAC AAG GCG GGC CTT TTG ACG      546
Ala His Thr Val Pro Lys Ile Asn Gly Asn Lys Ala Gly Leu Leu Thr
55                  60                  65                  70

CCT ATG GAG AGC ACT AAG GAC GAG GAC ATC GTG GCT GCC CCA ACG GTT      594
Pro Met Glu Ser Thr Lys Asp Glu Asp Ile Val Ala Ala Pro Thr Val
                75                  80                  85

GCT CCT AAG AGG ACT TTC ATC AAC CAG CTG CCG GAT TGG AGC ATG CTT      642
Ala Pro Lys Arg Thr Phe Ile Asn Gln Leu Pro Asp Trp Ser Met Leu
            90                  95                  100

CTT GCA GCA ATC ACA ACC ATC TTC TTG GCA GCC GAG AAG CAG TGG ACG      690
Leu Ala Ala Ile Thr Thr Ile Phe Leu Ala Ala Glu Lys Gln Trp Thr
        105                 110                 115

AAT CTT GAC TGG AAG CCC AGG AGG CCT GAC ATG CTC GTC GAC TTT GAC      738
Asn Leu Asp Trp Lys Pro Arg Arg Pro Asp Met Leu Val Asp Phe Asp
    120                 125                 130

CCT TTT AGT CTG GGG AGG TTC GTT CAG GAT GGG TTG ATT TTC AGG CAG      786
Pro Phe Ser Leu Gly Arg Phe Val Gln Asp Gly Leu Ile Phe Arg Gln
135                 140                 145                 150
```

FIG.3B

```
AAT TTC TCC ATC AGG TCT TAT GAG ATT GGC GCG GAT CGG ACG GCA TCC     834
Asn Phe Ser Ile Arg Ser Tyr Glu Ile Gly Ala Asp Arg Thr Ala Ser
                155                 160                 165

ATA GAG ACG TTA ATG AAT CAT CTA CAG GAA ACG GCC CTA AAC CAT GTA     882
Ile Glu Thr Leu Met Asn His Leu Gln Glu Thr Ala Leu Asn His Val
            170                 175                 180

AGG TGT ATA GGG CTC CTC GAT GAT GGT TTT GGT TCG ACG CCT GAG ATG     930
Arg Cys Ile Gly Leu Leu Asp Asp Gly Phe Gly Ser Thr Pro Glu Met
        185                 190                 195

ACT AGG AGA GAT CTG ATA TGG GTG GTT ACA AGG ATG CAG GTT CTG GTG     978
Thr Arg Arg Asp Leu Ile Trp Val Val Thr Arg Met Gln Val Leu Val
    200                 205                 210

GAT CGC TAT CCT TCC TGG GGG GAT GTC ATT GAA GTA GAC TCC TGG GTT    1026
Asp Arg Tyr Pro Ser Trp Gly Asp Val Ile Glu Val Asp Ser Trp Val
215                 220                 225                 230

ACT CCA TCT GGA AAG AAT GGG ATG AAA CGT GAA TGG TTT CTC CGT GAT    1074
Thr Pro Ser Gly Lys Asn Gly Met Lys Arg Glu Trp Phe Leu Arg Asp
                235                 240                 245

TGC AAG ACA GGC GAA ATC CTG ACA CGA GCT ACC AGT GTT TGG GTG ATG    1122
Cys Lys Thr Gly Glu Ile Leu Thr Arg Ala Thr Ser Val Trp Val Met
            250                 255                 260
```

FIG.3C

```
ATG AAT AAA CGG ACA CGG AGG TTG TCC AAA ATC CCT GAA GAA GTT AGA   1170
Met Asn Lys Arg Thr Arg Arg Leu Ser Lys Ile Pro Glu Glu Val Arg
        265                 270                 275
GTC GAA ATA GAG CCT TAT TTT GTG GAG CAT GGA GTC TTG GAT GAG GAC   1218
Val Glu Ile Glu Pro Tyr Phe Val Glu His Gly Val Leu Asp Glu Asp
    280                 285                 290

AGC AGA AAA CTA CCA AAG CTC AAT GAC AAC ACT GCA AAT TAC ATC AGA   1266
Ser Arg Lys Leu Pro Lys Leu Asn Asp Asn Thr Ala Asn Tyr Ile Arg
295                 300                 305                 310

AGA GGC CTA GCT CCT CGG TGG AGT GAT TTA GAT GTC AAT CAG CAT GTG   1314
Arg Gly Leu Ala Pro Arg Trp Ser Asp Leu Asp Val Asn Gln His Val
                315                 320                 325

AAC AAT GTC AAA TAC ATT GGC TGG ATT CTT GAG AGC GTG CCA TCT TCA   1362
Asn Asn Val Lys Tyr Ile Gly Trp Ile Leu Glu Ser Val Pro Ser Ser
            330                 335                 340

CTG TTG GAG AGT CAT GAG CTG TAT GGG ATG ACA CTT GAG TAT AGG AAG   1410
Leu Leu Glu Ser His Glu Leu Tyr Gly Met Thr Leu Glu Tyr Arg Lys
        345                 350                 355

GAG TGT GGA AAG GAC GGT TTG CTG CAA TCC CTG ACT GCT GTT GCC AGT   1458
Glu Cys Gly Lys Asp Gly Leu Leu Gln Ser Leu Thr Ala Val Ala Ser
    360                 365                 370
```

FIG.3D

```
GAT TAT GGG GGT GGA TCC CTT GAA GCT GGC GTT GAG TGT GAC CAC CTT   1506
Asp Tyr Gly Gly Gly Ser Leu Glu Ala Gly Val Glu Cys Asp His Leu
375                 380                 385                 390

CTT CGC CTT GAA GAT GGG AGT GAG ATT ATG AGG GGA AAG ACG GAA TGG   1554
Leu Arg Leu Glu Asp Gly Ser Glu Ile Met Arg Gly Lys Thr Glu Trp
                395                 400                 405

AGG CCC AAG CGT GCC GCC AAC ACT ACC TAC TTT GGA AGC GTT GAT GAT   1602
Arg Pro Lys Arg Ala Ala Asn Thr Thr Tyr Phe Gly Ser Val Asp Asp
            410                 415                 420

ATT CCT CCA GCA AAT AAT GCA TAGCCAAAAT GTATATATAT ATATATATAT      1653
Ile Pro Pro Ala Asn Asn Ala
        425

ATATATATAT ATATATATAT ATATATATAT ATTGGGTGGG GAGCAGCTGC AGCGGCAGCA 1713

GCACGACAAT GTCGAGGACA CGATGACGAT CAGTATGTTT CGTGCGGTAT TTAGCAATTC 1773

CGTATGTAGA ATCCTGCGTG TACTGGCAGA TAATTTTTTG ATTTGTTCTT TTCGTTTACG 1833

AGGGGAACCC GTGTAATTAG TTCAACTGTA TTTTCTGTTT CTTCCTTAAG TGTTTCAACA 1893
```

FIG.3E

CCCCTCTCTC TCTCGCGCGC GCGCGTGCGC TCACATTTTC CATTCCTTTT CTTTTTATTC 1953

TAGTTGTACG AGTGGGAGTT CATTTGCACT 1983

FIG.3F

```
T CTA GAG TGG AAG CCG AAG CCG AAT CCA CCC CAG TTG CTT GAT GAC CAT   49
  Leu Glu Trp Lys Pro Lys Pro Asn Pro Pro Gln Leu Leu Asp Asp His
  1               5                  10                  15

TTT GGG CCG CAT GGG TTA GTT TTC AGG CGC ACC TTT GCC ATC AGA TCG    97
Phe Gly Pro His Gly Leu Val Phe Arg Arg Thr Phe Ala Ile Arg Ser
            20                  25                  30

TAT GAG GTG GGA CCT GAC CGC TCC ACA TCT ATA GTG GCT GTT ATG AAT   145
Tyr Glu Val Gly Pro Asp Arg Ser Thr Ser Ile Val Ala Val Met Asn
        35                  40                  45

CAC TTG CAG GAG GCT GCA CTT AAT CAT GCG AAG AGT GTG GGA ATT CTA   193
His Leu Gln Glu Ala Ala Leu Asn His Ala Lys Ser Val Gly Ile Leu
    50                  55                  60

GGA GAT GGA TTC GGT ACG ACG CTA GAG ATG AGT AAG AGA GAT CTG ATA   241
Gly Asp Gly Phe Gly Thr Thr Leu Glu Met Ser Lys Arg Asp Leu Ile
65                  70                  75                  80

TGG GTT GTG AAA CGC ACG CAT GTT GCT GTG GAA CGG TAC CCT GCT TGG   289
Trp Val Val Lys Arg Thr His Val Ala Val Glu Arg Tyr Pro Ala Trp
                85                  90                  95

GGT GAT ACT GTT GAA GTA GAG TGC TGG GTT GGT GCA TCG GGA AAT AAT   337
Gly Asp Thr Val Glu Val Glu Cys Trp Val Gly Ala Ser Gly Asn Asn
            100                 105                 110
```

FIG.4A

```
GGC AGG CGC CAT GAT TTC CTT GTC CGG GAC TGC AAA ACA GGC GAA ATT     385
Gly Arg Arg His Asp Phe Leu Val Arg Asp Cys Lys Thr Gly Glu Ile
        115                 120                 125

CTT ACA AGA TGT ACC AGT CTT TCG GTG ATG ATG AAT ACA AGG ACA AGG     433
Leu Thr Arg Cys Thr Ser Leu Ser Val Met Met Asn Thr Arg Thr Arg
    130                 135                 140

AGG TTG TCC AAA ATC CCT GAA GAA GTT AGA GGG GAG ATA GGG CCT GCA     481
Arg Leu Ser Lys Ile Pro Glu Glu Val Arg Gly Glu Ile Gly Pro Ala
145                 150                 155                 160

TTC ATT GAT AAT GTG GCT GTC AAA GAC GAG GAA ATT AAG AAA CCA CAG     529
Phe Ile Asp Asn Val Ala Val Lys Asp Glu Glu Ile Lys Lys Pro Gln
                165                 170                 175

AAG CTC AAT GAC AGC ACT GCA GAT TAC ATC CAA GGA GGA TTG ACT CCT     577
Lys Leu Asn Asp Ser Thr Ala Asp Tyr Ile Gln Gly Gly Leu Thr Pro
            180                 185                 190

CGA TGG AAT GAT TTG GAT ATC AAT CAG CAC GTT AAC AAC ATC AAA TAC     625
Arg Trp Asn Asp Leu Asp Ile Asn Gln His Val Asn Asn Ile Lys Tyr
        195                 200                 205

GTT GAC TGG ATT CTT GAG ACT GTC CCA GAC TCA ATC TTT GAG AGT CAT     673
Val Asp Trp Ile Leu Glu Thr Val Pro Asp Ser Ile Phe Glu Ser His
    210                 215                 220
```

FIG.4B

```
CAT ATT TCC AGC TTC ACT ATT GAA TAC AGG AGA GAG TGC ACG AGG GAT      721
His Ile Ser Ser Phe Thr Ile Glu Tyr Arg Arg Glu Cys Thr Arg Asp
225                 230                 235                 240

AGC GTG CTG CAG TCC CTG ACC ACT GTC TCC GGT GGC TCG TCG GAA GCT      769
Ser Val Leu Gln Ser Leu Thr Thr Val Ser Gly Gly Ser Ser Glu Ala
                245                 250                 255

GGG TTA GTG TGC GAG CAC TTG CTC CAG CTT GAA GGT GGG TCT GAG GTA      817
Gly Leu Val Cys Glu His Leu Leu Gln Leu Glu Gly Gly Ser Glu Val
            260                 265                 270

TTG AGG GCA AAA ACA GAG TGG AGG CCT AAG CTT ACC GAT AGT TTC AGA      865
Leu Arg Ala Lys Thr Glu Trp Arg Pro Lys Leu Thr Asp Ser Phe Arg
        275                 280                 285

GGG ATT AGT GTG ATA CCC GCA GAA TCG AGT GTC TAACTAACGA AAGAAGCATC    918
Gly Ile Ser Val Ile Pro Ala Glu Ser Ser Val
    290                 295

TGATGAAGTT TCTCCTGTGC TGTTGTTCGT GAGGATGCTT TTTAGAAGCT GCAGTTTGCA    978

TTGCTTGTGC AGAATCATGG CCTGTGGTTT TAGATATATA TTCAAAATTG TCCTATAGTC   1038

AAGAAACTTA ATATCAGAAA AATAACTCAA TGAGTCAAGG TTATCGAAGT AGTCATGTAA   1098

GCTTTGAAAT ATGTTGTGTA TTCCTCGGCT TTATGTAATC TGTAAGCTCT TTCTCTTGC    1157
```

FIG.4C

```
GAA TTC GGC ACG AGG GGC TCC GGT GCT TTG CAG GTG AAG GCA AGT TCC      48
Glu Phe Gly Thr Arg Gly Ser Gly Ala Leu Gln Val Lys Ala Ser Ser
                5                  10                  15

CAA GCT CCA CCA AAG CTC AAT GGT TCC AAT GTG GGT TTG GTT AAA TCT      96
Gln Ala Pro Pro Lys Leu Asn Gly Ser Asn Val Gly Leu Val Lys Ser
            20                  25                  30

AGC CAA ATT GTG AAG AAG GGT GAT GAC ACC ACA TCT CCT CCT GCA AGA     144
Ser Gln Ile Val Lys Lys Gly Asp Asp Thr Thr Ser Pro Pro Ala Arg
        35                  40                  45

ACT TTC ATC AAC CAA TTG CCT GAT TGG AGC ATG CTT CTT GCT GCT ATC     192
Thr Phe Ile Asn Gln Leu Pro Asp Trp Ser Met Leu Leu Ala Ala Ile
    50                  55                  60

ACA ACC CTG TTC TTG GCT GCA GAG AAG CAG TGG ATG ATG CTT GAT TGG     240
Thr Thr Leu Phe Leu Ala Ala Glu Lys Gln Trp Met Met Leu Asp Trp
65                  70                  75                  80

AAA CCC AAA AGG CCT GAC ATG CTT GTT GAT CCA TTT GGT CTT GGA AGG     288
Lys Pro Lys Arg Pro Asp Met Leu Val Asp Pro Phe Gly Leu Gly Arg
                85                  90                  95

TTT GTT CAG GAT GGT CTT GTT TTC CGC AAC AAC TTT TCA ATT CGA TCA     336
Phe Val Gln Asp Gly Leu Val Phe Arg Asn Asn Phe Ser Ile Arg Ser
            100                 105                 110
```

FIG. 5A

```
TAT GAA ATA GGG GCT GAT CGA ACG GCT TCT ATA GAA ACG TTA ATG AAT      384
Tyr Glu Ile Gly Ala Asp Arg Thr Ala Ser Ile Glu Thr Leu Met Asn
        115                 120                 125

CAT CTG CAG GAA ACA GCT CTT AAT CAT GTG AAG TCT GTT GGG CTT CTT      432
His Leu Gln Glu Thr Ala Leu Asn His Val Lys Ser Val Gly Leu Leu
    130                 135                 140

GAG GAT GGC CTA GGT TCG ACT CGA GAG ATG TCC TTG AGG AAC CTG ATA      480
Glu Asp Gly Leu Gly Ser Thr Arg Glu Met Ser Leu Arg Asn Leu Ile
145                 150                 155                 160

TGG GTT GTC ACT AAA ATG CAG GTT GCG GTT GAT CGC TAT CCA ACT TGG      528
Trp Val Val Thr Lys Met Gln Val Ala Val Asp Arg Tyr Pro Thr Trp
                165                 170                 175

GGA GAT GAA GTT CAG GTA TCC TCT TGG GCT ACT GCA ATT GGA AAG AAT      576
Gly Asp Glu Val Gln Val Ser Ser Trp Ala Thr Ala Ile Gly Lys Asn
            180                 185                 190

GGA ATG CGT CGC GAA TGG ATA GTC ACT GAT TTT AGA ACT GGT GAA ACT      624
Gly Met Arg Arg Glu Trp Ile Val Thr Asp Phe Arg Thr Gly Glu Thr
        195                 200                 205

CTA TTA AGA GCC ACC AGT GTT TGG GTG ATG ATG AAT AAA CTG ACG AGG      672
Leu Leu Arg Ala Thr Ser Val Trp Val Met Met Asn Lys Leu Thr Arg
    210                 215                 220
```

FIG. 5B

```
AGG ATA TCC AAA ATC CCA GAA GAG GTT TGG CAC GAA ATA GGC CCC TCT      720
Arg Ile Ser Lys Ile Pro Glu Glu Val Trp His Glu Ile Gly Pro Ser
225                 230                 235                 240

TTC ATT GAT GCT CCT CCT CTT CCC ACC GTG GAA GAT GAT GGT AGA AAG      768
Phe Ile Asp Ala Pro Pro Leu Pro Thr Val Glu Asp Asp Gly Arg Lys
                245                 250                 255

CTG ACA AGG TTT GAT GAA AGT TCT GCA GAC TTT ATC CGC NCT GGT TTA      816
Leu Thr Arg Phe Asp Glu Ser Ser Ala Asp Phe Ile Arg Xxx Gly Leu
            260                 265                 270

ACT CCT AGG TGG AGT GAT TTG GAC ATC AAC CAG CAT GTC AAC AAT GTG      864
Thr Pro Arg Trp Ser Asp Leu Asp Ile Asn Gln His Val Asn Asn Val
        275                 280                 285

AAG TAC ATT GGC TGG CTC CTT GAG AGT GCT CCG CCG GAG ATC CAC GAG      912
Lys Tyr Ile Gly Trp Leu Leu Glu Ser Ala Pro Pro Glu Ile His Glu
    290                 295                 300

AGT CAC GAG ATA GCG TCT CTG ACT CTG GAG TAC AGG AGG GAG TGT GGA      960
Ser His Glu Ile Ala Ser Leu Thr Leu Glu Tyr Arg Arg Glu Cys Gly
305                 310                 315                 320

AGG GAC AGC GTG CTG AAC TCC GCG ACC AAG GTC TCT GAC TCC TCT CAA     1008
Arg Asp Ser Val Leu Asn Ser Ala Thr Lys Val Ser Asp Ser Ser Gln
                325                 330                 335
```

FIG. 5C

```
CTG GGA AAG TCT GCT GTG GAG TGT AAC CAC TTG GTT CGT CTC CAG AAT   1056
Leu Gly Lys Ser Ala Val Glu Cys Asn His Leu Val Arg Leu Gln Asn
            340                 345                 350

GGT GGG GAG ATT GTG AAG GGA AGG ACT GTG TGG AGG CCC AAA CGT CCT   1104
Gly Gly Glu Ile Val Lys Gly Arg Thr Val Trp Arg Pro Lys Arg Pro
        355                 360                 365

CTT TAC AAT GAT GGT GCT GTT GTG GAC GTG NAA GCT AAA ACC TCT       1149
Leu Tyr Asn Asp Gly Ala Val Val Asp Val Xxx Ala Lys Thr Ser
    370                 375                 380

TAAGTCTTAT AGTCCAAGTG AGGAGGAGTT CTATGTATCA GGAAGTTGCT AGGATTCTCA 1209

ATCGCATGTG TCCATTTCTT GTGTGGAATA CTGCTCGTGT TTCTAGACTC GCTATATGTT 1269

TGTTCTTTTA TATATATATA TATATATATA TCTCTCTCTT CCCCCCACCT CTCTCTCTCT 1329

CTCTATATAT ATATATGTTT TATGTAAGTT TTCCCCTTAG TTTCCTTTCC TAAGTAATGC 1389

CATTGTAAAT TACTTCAAAA AAAAAAAAAA AAAAAAAACT CGAG                  1433
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FIG. 5D

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GGCACGAGAA ACATGGTGGC TGCCGCAGCA AGTTCTGCAT TCTTCTCCGT TCCAACCCCG   60

GGAATCTCCC CTAAACCCGG GAAGTTCGGT AATGGTGGCT TTCAGGTTAA GGCAAACGCC  120

AATGCCCATC CTAGTCTAAA GTCTGGCAGC CTCGAGACTG AAGATGACAC TTCATCGTCG  180

TCCCCTCCTC CTCGGACTTT CATTAACCAG TTGCCCGACT GGAGTATGCT TCTGTCCGCA  240

ATCACGACTA TCTTCGGGGC AGCTGAGAAG CAGTGGATGA TGCTTGATAG GAAATCTAAG  300

NAGACCCGAC ATGCTCATGG CAACCGTTTG GGGTTGACAG TATTGTTCAG GATGGGGTTT  360

TTTTCAGACA GAGTTTTTCG ATTAGATCTT ACGAAATAGG CGCTGATCGA ACAACCTCAA  420

TAGAGACGCT GATGAACATG TTCCAGGAAA CGTCTTTGAA TCATTGTAAG AGTAACGGTC  480

TTCTCAATGA CGGCTTTGGT CGCACTCCTG AGATGTGTAA GAAGGGCCTC ATTTGGGTGG  540

TTACGAAAAT GCAGGTCGAG GTGAATCGCT ATCCTATTTG GSGTGATTCT ATCGAAGTCA  600

ATACTTGGGT CTCCGAGTCG GGGNAAAANC GGTATGGGTC GTGATTGGCT GATAAGTGAT  660
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FIG.6A

TGCAGTACAG GAGNAAATTC TTGTAAGAGC AACGAGCGTG TGGGCTATGA TGAATCAAAA 720

GACGAGAAGA TTGTCAAAAT TTCCATTTGA GGTTCGACAA GAGATAGCGC CTAATTTTGT 780

CGACTCTGTT CCTGTCATTG AAGACGATCG AAAATTACAC AAGCTTGATG TGAAGACGGG 840

TGATTCCATT CACAATGGTC TAACTCCAAG GTGGAATGAC TTGGATGTCA ATCAGCACGT 900

TAACAATGTG AAATACATTG GGTGGATTCT CAAGAGTGTT CCAACAGATG TTTTTGGGGC 960

CCAGGAGCTA TGTGGA 976

FIG.6B

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GGCGCGCCGG TACCTCTAGA CCTGGCGATT CAACGTGGTC GGATCATGAC GCTTCCAGAA    60

AACATCGAGC AAGCTCTCAA AGCTGACCTC TTTCGGATCG TACTGAACCC GAACAATCTC   120

GTTATGTCCC GTCGTCTCCG AACAGACATC CTCGTAGCTC GGATTATCGA CGAATCCATG   180

GCTATACCCA ACCTCCGTCT TCGTCACGCC TGGAACCCTC TGGTACGCCA ATTCCGCTCC   240

CCAGAAGCAA CCGGCGCCGA ATTGCGCGAA TTGCTGACCT GGAGACGGAA CATCGTCGTC   300

GGGTCCTTGC GCGATTGCGG CGGAAGCCGG GTCGGGTTGG GGACGAGACC CGAATCCGAG   360

CCTGGTGAAG AGGTTGTTCA TCGGAGATTT ATAGACGGAG ATGGATCGAG CGGTTTTGGG   420

GAAAGGGGAA GTGGGTTTGG CTCTTTTGGA TAGAGAGAGT GCAGCTTTGG AGAGAGACTG   480

GAGAGGTTTA GAGAGAGACG CGGCGGATAT TACCGGAGGA GAGGCGACGA GAGATAGCAT   540

TATCGAAGGG GAGGGAGAAA GAGTGACGTG GAGAAATAAG AAACCGTTAA GAGTCGGATA   600
```

FIG. 7A

TTTATCATAT TAAAAGCCCA ATGGGCCTGA ACCCATTTAA ACAAGACAGA TAAATGGGCC 660

GTGTGTTAAG TTAACAGAGT GTTAACGTTC GGTTTCAAAT GCCAACGCCA TAGGAACAAA 720

ACAAACGTGT CCTCAAGTAA ACCCCTGCCG TTTACACCTC AATGGCTGCA TGGTGAAGCC 780

ATTAACACGT GGCGTAGGAT GCATGACGAC GCCATTGACA CCTGACTCTC TTCCCTTCTC 840

TTCATATATC TCTAATCAAT TCAACTACTC ATTGTCATAG CTATTCGGAA AATACATACA 900

CATCCTTTTC TCTTCGATCT CTCTCAATTC ACAAGAAGCA AAGTCGACGG ATCCCTGCAG 960

TAAATTACGC CATGACTATT TTCATAGTCC AATAAGGCTG ATGTCGGGAG TCCAGTTTAT 1020

GAGCAATAAG GTGTTTAGAA TTTGATCAAT GTTTATAATA AAAGGGGGAA GATGATATCA 1080

CAGTCTTTTG TTCTTTTTGG CTTTTGTTAA ATTTGTGTGT TTCTATTTGT AAACCTCCTG 1140

TATATGTTGT ACTTCTTTCC CTTTTTAAGT GGTATCGTCT ATATGGTAAA ACGTTATGTT 1200

FIG. 7B

```
TGGTCTTTCC TTTTCTCTGT TTAGGATAAA AAGACTGCAT GTTTTATCTT TAGTTATATT  1260

ATGTTGAGTA AATGAACTTT CATAGATCTG GTTCCGTAGA GTAGACTAGC AGCCGAGCTG  1320

AGCTGAACTG AACAGCTGGC AATGTGAACA CTGGATGCAA GATCAGATGT GAAGATCTCT  1380

AATATGGTGG TGGGATTGAA CATATCGTGT CTATATTTTT GTTGGCATTA AGCTCTTAAC  1440

ATAGATATAA CTGATGCAGT CATTGGTTCA TACACATATA TAGTAAGGAA TTACAATGGC  1500

AACCCAAACT TCAAAAACAG TAGGCCACCT GAATTGCCTT ATCGAATAAG AGTTTGTTTC  1560

CCCCCACTTC ATGGGATGTA ATACATGGGA TTTGGGAGTT TGAATGAACG TTGAGACATG  1620

GCAGAACCTC TAGAGGTACC GGCGCGC                                      1647
```

FIG. 7C

SAMPLE	% 8:0	%10:0	%12:0	%14:0	%16:0	%16:1	%18:0	%18:1	%18:2	%18:3	%20:0	%20:1	%20:2	%22:0	%22:1	%22:2
3854-3	0.00	1.84	0.03	0.07	4.54	0.21	2.62	69.78	17.22	1.34	0.78	1.16	0.04	0.38	0.00	0.00
3854-3	0.00	1.53	0.12	7.63	21.94	0.25	7.00	44.67	12.99	1.00	1.65	0.65	0.01	0.57	0.00	0.00
3854-3	0.00	0.15	0.27	16.40	31.31	0.45	7.02	25.70	15.12	0.91	1.78	0.36	0.00	0.51	0.00	0.00
3854-3	0.00	0.80	0.22	14.53	29.02	0.37	7.05	29.67	14.58	0.96	1.81	0.45	0.01	0.54	0.00	0.00
3854-3	0.00	1.46	0.30	18.86	32.21	0.31	7.50	22.53	12.67	0.85	2.26	0.33	0.01	0.71	0.00	0.00
3854-3	0.00	3.94	0.28	15.46	28.46	0.49	7.09	26.38	14.72	0.92	1.58	0.29	0.00	0.38	0.00	0.01
3854-3	0.00	2.15	0.24	19.46	33.03	0.20	6.19	23.09	11.66	0.93	2.06	0.31	0.00	0.68	0.00	0.00
3854-3	0.00	3.81	0.12	16.79	32.73	0.35	7.69	23.07	10.83	0.96	2.54	0.26	0.00	0.86	0.00	0.00
3854-3	0.00	6.40	0.38	20.90	30.38	0.41	6.27	21.28	10.61	0.90	1.79	0.22	0.02	0.40	0.01	0.00
3854-3	0.00	6.28	0.45	23.89	37.77	0.37	9.59	13.52	4.02	0.23	2.47	0.60	0.00	0.81	0.00	0.00
3854-3	0.00	1.04	0.04	0.09	4.49	0.11	2.31	69.29	18.94	1.42	0.75	1.19	0.02	0.31	0.00	0.00
3854-3	0.00	3.04	0.18	19.35	32.37	0.31	7.35	22.76	10.24	0.98	2.35	0.29	0.00	0.76	0.01	0.00
3854-11	0.00	1.39	0.33	17.95	30.29	0.66	6.77	23.35	15.37	1.03	1.87	0.35	0.01	0.62	0.00	0.00
3854-11	0.00	1.93	0.36	21.31	31.37	0.34	6.09	22.92	12.38	1.05	1.96	0.06	0.02	0.20	0.01	0.00
3854-11	0.00	1.22	0.27	18.75	31.33	0.50	6.91	25.50	13.08	0.89	1.12	0.31	0.01	0.11	0.01	0.01
3854-11	0.00	1.53	0.23	17.30	33.28	0.56	1.25	29.63	14.07	0.41	0.90	0.30	0.01	0.49	0.00	0.04
3854-11	0.00	0.50	0.03	0.04	3.93	0.07	2.92	76.55	12.30	0.99	0.95	1.27	0.02	0.42	0.01	0.00
3854-11	0.00	0.91	0.35	16.96	30.43	0.45	7.67	25.02	15.14	0.85	1.57	0.31	0.00	0.34	0.00	0.00
3854-11	0.00	1.44	0.38	23.03	33.37	0.45	7.07	19.31	11.50	0.98	1.73	0.23	0.00	0.52	0.01	0.00
3854-11	0.00	2.17	0.30	18.27	32.78	0.43	7.17	24.74	10.03	0.82	2.30	0.29	0.01	0.70	0.00	0.00
3854-11	0.00	1.73	0.29	21.83	32.82	0.30	7.41	20.85	11.18	0.71	2.07	0.19	0.00	0.61	0.00	0.00
3854-11	0.00	1.50	0.42	23.00	32.88	0.42	6.86	17.89	13.69	0.86	1.74	0.23	0.00	0.50	0.00	0.00
3854-11	0.00	2.16	0.34	21.37	36.03	0.27	8.12	19.29	8.56	0.60	2.25	0.25	0.00	0.75	0.01	0.00
3854-11	0.00	2.71	0.32	20.56	33.43	0.79	7.70	20.91	10.42	0.88	1.66	0.17	0.01	0.44	0.00	0.00

Figure 8

SAMPLE	% 8:0	%10:0	%12:0	%14:0	%16:0	%16:1	%18:0	%18:1	%18:2	%18:3	%20:0	%20:1	%20:2	%22:0	%22:1	%22:2
5233-5	0.00	0.00	1.01	10.88	12.07	0.45	1.63	45.12	15.93	12.05	0.22	0.66	0.00	0.00	0.00	0.00
5233-5	0.00	0.00	0.62	6.78	10.89	0.42	1.52	48.26	16.45	14.04	0.31	0.71	0.00	0.00	0.00	0.00
5233-5	0.00	0.00	0.32	5.22	11.15	0.62	1.33	46.32	19.06	14.81	0.38	0.79	0.00	0.00	0.00	0.00
5233-5	0.00	0.00	1.10	11.92	13.11	0.48	1.17	41.16	18.63	12.06	0.08	0.22	0.06	0.00	0.00	0.00
5233-5	0.00	0.00	0.47	6.39	12.06	0.49	1.55	44.78	20.34	13.11	0.16	0.62	0.00	0.05	0.00	0.00
5233-5	0.00	0.00	1.60	14.96	13.99	0.46	1.26	38.28	16.52	12.19	0.09	0.61	0.00	0.00	0.05	0.00
5233-5	0.00	0.00	1.74	15.07	12.96	0.46	1.48	40.24	15.80	11.54	0.08	0.54	0.00	0.00	0.03	0.03
5233-5	0.00	0.00	1.21	12.56	12.78	0.48	1.48	43.93	14.62	11.86	0.33	0.76	0.00	0.00	0.00	0.00
5233-5	0.00	0.00	0.97	11.85	14.12	0.56	1.23	41.07	17.69	11.87	0.08	0.49	0.00	0.04	0.00	0.04
5233-5	0.00	0.00	0.83	8.97	12.39	0.42	1.58	48.28	16.85	9.56	0.34	0.69	0.04	0.06	0.00	0.00
5233-5	0.00	0.00	0.93	10.31	12.40	0.48	1.79	47.27	14.61	11.15	0.33	0.67	0.00	0.00	0.04	0.00
5233-5	1.84	0.00	0.08	0.13	7.23	0.17	1.62	53.76	19.19	14.81	0.31	0.85	0.00	0.00	0.00	0.00
5233-5	0.00	0.00	1.08	11.33	11.69	0.41	1.37	48.20	13.69	11.39	0.25	0.57	0.00	0.04	0.00	0.00
5233-5	0.00	0.00	0.92	11.49	13.95	0.63	1.15	39.54	18.18	13.09	0.24	0.68	0.08	0.01	0.00	0.03
5233-5	0.00	0.00	0.63	8.78	12.57	0.33	1.10	43.92	18.31	13.42	0.19	0.67	0.07	0.00	0.00	0.00
5233-5	0.00	0.00	1.80	17.17	14.47	0.54	1.23	38.34	15.29	10.44	0.14	0.56	0.00	0.00	0.00	0.01
5233-5	0.00	0.00	1.95	17.01	14.57	0.70	1.29	35.66	17.51	10.43	0.21	0.64	0.02	0.00	0.00	0.00
5233-5	0.00	0.00	0.87	11.22	13.23	0.40	1.29	40.45	18.98	12.75	0.16	0.54	0.00	0.09	0.02	0.00
5233-5	0.00	0.00	1.03	11.39	12.29	0.41	1.70	44.98	14.84	11.99	0.43	0.83	0.02	0.03	0.02	0.03
5233-5	0.00	0.00	0.76	8.93	13.19	0.20	1.26	41.27	19.80	14.12	0.07	0.34	0.00	0.00	0.08	0.00
5233-5	0.00	0.00	1.10	11.90	11.95	0.46	1.68	45.86	13.59	12.37	0.32	0.72	0.00	0.04	0.00	0.00
5233-5	0.00	0.00	1.05	10.72	12.43	0.44	1.49	43.90	15.96	13.12	0.15	0.70	0.00	0.05	0.00	0.00
5233-5	0.00	0.00	1.04	11.64	12.34	0.44	1.66	45.20	14.22	12.35	0.31	0.69	0.04	0.07	0.00	0.00
5233-5	0.00	0.37	0.45	4.76	11.20	0.12	0.94	45.76	21.36	14.10	0.09	0.83	0.00	0.02	0.00	0.00
5233-5	0.00	0.00	1.51	15.42	14.10	0.53	1.48	39.41	14.68	12.21	0.08	0.58	0.00	0.00	0.02	0.00

Figure 9A

SAMPLE	% 8:0	%10:0	%12:0	%14:0	%16:0	%16:1	%18:0	%18:1	%18:2	%18:3	%20:0	%20:1	%20:2	%22:0	%22:1	%22:2
5233-6	0.00	0.19	1.60	15.35	13.19	0.53	1.33	41.03	14.00	11.85	0.15	0.76	0.00	0.00	0.00	0.03
5233-6	0.00	0.00	1.37	15.02	13.03	0.53	1.57	42.48	12.42	12.59	0.30	0.68	0.00	0.00	0.00	0.02
5233-6	0.00	0.00	1.32	13.77	12.79	0.41	1.26	42.40	14.19	12.80	0.27	0.80	0.00	0.00	0.00	0.00
5233-6	0.00	0.00	1.37	14.16	12.64	0.30	1.39	43.59	13.27	12.30	0.29	0.60	0.02	0.01	0.00	0.03
5233-6	0.00	0.00	2.05	18.99	14.48	0.41	1.22	37.18	13.57	11.46	0.14	0.47	0.03	0.00	0.00	0.00
5233-6	0.00	0.00	0.75	8.54	12.62	0.43	1.37	46.23	18.76	10.22	0.39	0.66	0.00	0.00	0.00	0.04
5233-6	0.00	0.00	0.18	2.53	9.04	0.19	1.53	52.87	17.70	14.68	0.33	0.92	0.00	0.02	0.01	0.00
5233-6	0.00	0.00	0.15	2.93	10.02	0.26	1.28	49.86	21.85	12.61	0.28	0.78	0.00	0.00	0.00	0.00
5233-6	0.00	0.00	1.95	17.52	13.40	0.55	1.54	40.26	12.87	10.98	0.25	0.66	0.02	0.00	0.00	0.00
5233-6	0.00	0.00	0.00	0.13	7.85	0.19	1.46	54.44	19.60	15.01	0.31	0.91	0.05	0.07	0.00	0.00
5233-6	0.00	0.00	1.25	12.71	12.78	0.53	1.06	42.38	15.85	12.75	0.20	0.39	0.04	0.04	0.00	0.00
5233-6	0.00	0.00	1.61	16.02	13.44	0.49	1.43	40.44	13.83	11.73	0.32	0.70	0.00	0.00	0.00	0.00
5233-6	0.00	0.28	0.48	5.65	10.20	0.32	1.61	50.49	16.71	13.30	0.19	0.76	0.00	0.00	0.00	0.00
5233-6	0.00	0.13	1.55	15.42	13.48	0.41	1.40	40.74	13.95	11.79	0.29	0.79	0.02	0.03	0.00	0.00
5233-6	0.00	0.00	1.06	10.96	12.39	0.53	1.54	42.30	16.35	13.76	0.30	0.77	0.02	0.03	0.00	0.00
5233-6	0.00	0.00	1.59	15.50	13.40	0.44	1.31	39.72	15.62	11.50	0.19	0.67	0.00	0.06	0.00	0.00
5233-6	0.00	0.00	2.62	21.42	14.67	0.42	1.32	35.45	12.71	10.61	0.17	0.57	0.03	0.02	0.00	0.00
5233-6	0.00	0.00	1.46	14.23	12.72	0.44	1.31	42.86	13.86	12.19	0.25	0.58	0.10	0.00	0.00	0.00
5233-6	0.99	0.00	2.47	20.66	14.57	0.47	1.25	34.24	13.72	10.78	0.15	0.56	0.08	0.03	0.01	0.00
5233-6	0.00	0.36	0.00	0.22	7.73	0.18	1.35	53.50	20.65	15.16	0.16	0.71	0.00	0.00	0.00	0.00
5233-6	0.22	1.00	0.40	5.08	9.95	0.25	1.26	50.05	16.93	13.69	0.21	0.87	0.02	0.00	0.03	0.05
5233-6	0.00	0.00	2.73	20.62	14.73	0.52	1.50	35.20	14.55	9.33	0.22	0.55	0.00	0.05	0.00	0.00
5233-6	0.53	0.32	1.60	14.10	12.18	0.51	1.39	43.88	12.56	12.27	0.30	0.34	0.03	0.00	0.00	0.00
5233-6	2.04	0.21	0.07	0.53	8.51	0.13	0.82	48.89	22.20	15.42	0.39	0.52	0.06	0.05	0.11	0.06
5233-6	0.29	0.45	1.66	15.50	12.49	0.33	0.27	44.04	12.90	11.39	0.07	0.52	0.04	0.02	0.02	0.03

Figure 9B

SAMPLE	%8:0	%10:0	%12:0	%14:0	%16:0	%16:1	%18:0	%18:1	%18:2	%18:3	%20:0	%20:1	%20:2	%22:0	%22:1	%22:2
3863-10	0.00	0.00	0.23	36.72	21.59	0.17	1.66	20.65	16.21	1.38	0.65	0.46	0.02	0.25	0.01	0.01
3863-10	0.00	0.00	0.33	42.87	18.70	0.30	1.72	18.86	14.79	1.36	0.57	0.40	0.02	0.05	0.01	0.01
3863-10	0.00	0.00	0.24	36.56	19.03	0.29	1.76	22.75	16.47	1.74	0.58	0.39	0.02	0.15	0.01	0.01
3863-10	0.00	0.00	0.32	42.65	19.06	0.33	2.26	18.58	14.01	1.43	0.68	0.33	0.03	0.27	0.02	0.03
3863-10	0.00	0.00	0.33	42.48	19.74	0.40	2.34	18.72	13.55	1.38	0.66	0.27	0.05	0.06	0.01	0.02
3863-10	0.00	0.00	0.33	42.88	18.88	0.30	1.95	17.73	15.44	1.44	0.64	0.27	0.04	0.08	0.02	0.01
3863-10	0.00	0.00	0.22	40.89	20.63	0.24	1.81	17.77	15.76	1.39	0.65	0.35	0.06	0.22	0.01	0.01
3863-10	0.00	0.00	0.20	29.49	17.06	0.24	1.86	28.63	19.46	1.68	0.58	0.66	0.05	0.06	0.01	0.02
3863-10	0.00	0.00	0.39	41.52	18.34	0.32	2.15	19.57	15.19	1.54	0.56	0.31	0.03	0.07	0.00	0.02
3863-10	0.00	0.00	0.30	37.55	20.00	0.23	1.79	23.58	13.87	1.47	0.59	0.51	0.03	0.05	0.02	0.02
3863-10	0.00	0.00	0.13	21.84	17.17	0.25	2.50	37.17	17.07	1.80	0.75	0.80	0.12	0.38	0.02	0.02
3863-10	0.00	0.00	0.14	25.13	17.66	0.23	2.00	31.52	20.07	1.42	0.65	0.81	0.05	0.29	0.01	0.00
3863-7	0.00	0.00	0.18	21.00	15.58	0.42	2.80	37.13	18.53	2.66	0.87	0.47	0.07	0.23	0.04	0.02
3863-7	0.00	0.00	0.14	16.64	14.67	0.38	2.99	38.90	21.75	2.91	0.81	0.56	0.08	0.13	0.03	0.02
3863-7	0.00	0.00	0.12	18.54	15.25	0.37	3.11	39.03	19.32	2.58	0.88	0.58	0.05	0.12	0.04	0.02
3863-7	0.00	0.00	0.12	18.55	14.81	0.38	3.16	37.62	20.65	3.20	0.82	0.42	0.02	0.19	0.03	0.02
3863-7	0.00	0.00	0.02	0.16	6.07	0.35	3.12	63.30	22.03	2.68	0.96	1.06	0.03	0.15	0.02	0.05
3863-7	0.00	0.00	0.14	16.90	14.90	0.41	2.97	40.23	20.11	2.83	0.79	0.63	0.05	0.02	0.01	0.02
3863-7	0.00	0.00	0.15	12.57	13.66	0.57	3.48	44.45	20.42	3.07	0.98	0.48	0.02	0.10	0.03	0.02
3863-7	0.00	0.00	0.11	10.22	12.64	0.58	3.83	46.53	20.86	3.35	1.14	0.46	0.03	0.19	0.03	0.04
3863-7	0.00	0.00	0.09	15.48	14.28	0.83	3.00	39.64	21.56	3.77	0.76	0.39	0.04	0.04	0.05	0.05
3863-7	0.00	0.00	0.08	10.89	12.79	0.54	3.00	46.69	21.23	3.54	0.76	0.29	0.04	0.03	0.09	0.03
3863-7	0.00	0.00	0.14	9.77	12.73	0.51	3.74	46.96	20.90	3.37	1.02	0.50	0.04	0.26	0.04	0.01
3863-7	0.00	0.00	0.16	15.86	14.25	0.51	3.46	41.12	19.50	3.32	0.89	0.60	0.07	0.17	0.03	0.04
3863-4	0.00	0.00	0.17	15.69	14.91	1.21	2.32	31.36	29.72	3.01	0.85	0.49	0.05	0.14	0.05	0.02
3863-4	0.00	0.00	0.23	38.63	19.96	0.29	1.41	20.94	15.70	1.39	0.62	0.54	0.03	0.25	0.01	0.01
3863-4	0.00	0.00	0.00	25.75	33.27	0.11	8.98	7.98	3.42	0.06	2.33	17.44	0.08	0.18	0.13	0.27
3863-4	0.00	0.00	0.17	30.59	19.06	0.26	1.70	27.57	17.30	1.41	0.76	0.74	0.04	0.38	0.01	0.01
3863-4	0.00	0.00	0.16	28.93	17.51	0.27	2.25	28.14	19.06	1.87	0.78	0.59	0.04	0.39	0.01	0.01
3863-4	0.00	0.00	0.19	31.48	18.44	0.21	2.06	28.98	15.77	1.37	0.71	0.65	0.03	0.09	0.01	0.01
3863-4	0.00	0.00	0.18	38.07	21.62	0.22	1.55	22.37	13.14	1.11	0.79	0.52	0.03	0.39	0.01	0.00

FIGURE 10A

SAMPLE	%8:0	%10:0	%12:0	%14:0	%16:0	%16:1	%18:0	%18:1	%18:2	%18:3	%20:0	%20:1	%20:2	%22:0	%22:1	%22:2
3863-4	0.00	0.00	0.18	29.22	18.35	0.34	2.02	29.70	16.70	1.58	0.74	0.79	0.06	0.29	0.01	0.01
3863-4	0.00	0.00	0.23	34.61	19.74	0.17	1.70	24.07	16.55	1.21	0.70	0.65	0.04	0.31	0.01	0.01
3863-4	0.00	0.00	0.18	30.56	18.47	0.19	2.08	28.61	16.81	1.50	0.68	0.63	0.04	0.24	0.01	0.01
3863-4	0.00	0.00	0.21	37.45	21.35	0.19	1.61	23.60	12.97	1.07	0.71	0.54	0.03	0.25	0.01	0.01
3863-4	0.00	0.00	0.18	29.70	18.98	0.19	2.03	29.00	16.70	1.36	0.77	0.73	0.00	0.36	0.01	0.01
3863-4	0.00	0.00	0.22	37.87	20.27	0.23	1.93	22.06	14.51	1.31	0.77	0.48	0.02	0.31	0.01	0.01
3863-4	0.00	0.00	0.21	39.14	21.36	0.19	1.64	21.46	13.42	1.13	0.69	0.37	0.09	0.30	0.01	0.00
3863-4	0.00	0.00	0.20	38.94	20.69	0.25	1.38	18.57	17.11	1.37	0.67	0.39	0.04	0.36	0.01	0.01
3863-4	0.00	0.00	0.01	0.21	5.81	0.32	4.29	65.31	18.68	2.19	1.38	1.19	0.01	0.59	0.01	0.01
3863-4	0.00	0.00	0.07	0.17	8.14	0.61	4.97	54.61	25.74	3.28	1.50	0.67	0.05	0.14	0.04	0.02
3863-4	0.00	0.00	0.16	30.31	19.06	0.26	1.92	27.23	17.65	1.58	0.76	0.72	0.03	0.32	0.00	0.01
3863-4	0.00	0.00	0.20	32.77	18.77	0.23	1.92	27.37	15.76	1.35	0.66	0.67	0.02	0.26	0.01	0.01
3863-4	0.00	0.00	0.28	37.97	19.58	0.34	1.74	21.75	15.46	1.60	0.66	0.46	0.03	0.10	0.01	0.01
3863-4	0.00	0.00	0.25	39.54	19.76	0.26	1.79	19.97	15.78	1.50	0.63	0.39	0.01	0.10	0.00	0.01
3863-4	0.00	0.00	0.19	31.46	18.50	0.17	2.00	30.06	14.81	1.30	0.75	0.66	0.01	0.07	0.01	0.01
3863-4	0.00	0.00	0.23	34.79	19.64	0.38	1.96	22.66	17.04	1.78	0.85	0.49	0.03	0.10	0.02	0.01
3863-4	0.00	0.00	0.21	31.55	18.70	0.23	2.16	27.97	15.73	1.44	0.83	0.70	0.04	0.40	0.01	0.01
3863-4	0.00	0.00	0.18	29.27	18.66	0.25	2.22	31.60	14.42	1.74	0.79	0.76	0.04	0.08	0.01	0.00
3863-4	0.00	0.00	0.58	50.92	32.69	0.46	4.72	5.73	2.75	0.16	1.17	0.39	0.06	0.28	0.05	0.05
3863-4	0.00	0.00	0.28	40.26	19.58	0.20	1.48	20.62	15.20	1.24	0.58	0.48	0.04	0.05	0.01	0.00
3863-4	0.00	0.00	0.20	32.09	18.27	0.17	2.03	28.26	15.99	1.43	0.71	0.74	0.04	0.05	0.01	0.01
3863-4	0.00	0.00	0.04	0.38	4.65	0.26	3.07	62.89	24.59	1.83	0.85	1.12	0.01	0.26	0.04	0.01
3863-4	0.00	0.00	0.19	30.34	18.77	0.28	1.83	25.81	19.41	1.46	0.73	0.77	0.03	0.36	0.01	0.02
3863-4	0.00	0.00	0.03	0.38	5.07	0.29	3.36	64.47	22.34	1.91	0.95	1.09	0.05	0.04	0.00	0.01
3863-4	0.00	0.00	0.22	37.53	20.33	0.30	1.87	21.73	15.14	1.30	0.80	0.46	0.03	0.29	0.01	0.01
3863-4	0.00	0.00	0.00	0.38	5.09	0.31	3.37	66.30	20.02	1.78	1.03	1.17	0.02	0.52	0.01	0.01
3863-4	0.00	0.00	0.02	0.38	4.79	0.23	3.87	68.32	17.76	1.98	1.07	1.16	0.01	0.37	0.02	0.01
3863-4	0.00	0.00	0.17	25.22	18.00	0.35	2.59	34.34	15.42	1.65	0.99	0.74	0.02	0.47	0.02	0.02
3863-4	0.00	0.00	0.17	29.76	18.99	0.21	2.32	31.59	13.69	1.20	0.86	0.78	0.04	0.38	0.01	0.01
3863-4	0.00	0.00	0.03	0.43	4.99	0.28	3.24	64.01	22.34	2.08	0.98	1.16	0.03	0.41	0.01	0.01
3863-8	0.00	0.00	0.02	0.10	5.32	0.31	3.67	61.45	24.35	2.55	0.96	1.14	0.02	0.09	0.01	0.02

FIGURE 10B

SAMPLE	%8:0	%10:0	%12:0	%14:0	%16:0	%16:1	%18:0	%18:1	%18:2	%18:3	%20:0	%20:1	%20:2	%22:0	%22:1	%22:2
3863-8	0.00	0.00	0.03	0.10	5.94	0.38	3.09	56.78	28.77	2.79	0.89	0.99	0.04	0.15	0.03	0.01
3863-8	0.00	0.00	0.04	0.14	5.78	0.36	3.44	64.06	21.60	2.45	0.91	1.02	0.02	0.15	0.02	0.02
3863-8	0.00	0.00	0.04	0.09	5.37	0.33	3.45	63.65	22.77	2.20	0.90	0.99	0.04	0.15	0.01	0.01
3863-8	0.00	0.00	0.08	0.09	6.57	0.45	4.04	58.85	24.60	3.22	1.00	0.84	0.04	0.19	0.02	0.02
3863-8	0.00	0.00	0.03	0.07	5.61	0.32	3.45	60.39	25.33	2.63	1.02	1.02	0.04	0.07	0.02	0.02
3863-8	0.00	0.00	0.02	0.12	5.80	0.42	3.87	66.16	18.67	2.47	1.03	0.89	0.10	0.40	0.01	0.02
3863-8	0.00	0.00	0.03	0.09	5.52	0.33	3.26	61.36	24.50	2.43	0.93	1.07	0.03	0.45	0.01	0.01
3863-8	0.00	0.00	0.02	0.15	5.25	0.25	3.14	62.11	24.32	2.41	0.85	1.08	0.04	0.36	0.01	0.01
3863-8	0.00	0.00	0.04	0.19	6.47	0.43	4.15	56.05	27.43	2.97	1.12	0.84	0.02	0.25	0.02	0.01
3863-8	0.00	0.00	0.03	0.16	6.13	0.38	3.48	59.94	24.95	2.68	0.97	0.86	0.05	0.33	0.02	0.01
3863-8	0.00	0.00	0.03	0.09	5.65	0.36	3.71	61.34	24.00	2.58	0.98	1.00	0.08	0.18	0.01	0.01
3863-2	0.00	0.00	0.22	26.95	17.05	0.28	2.31	32.94	15.90	2.37	0.84	0.64	0.11	0.36	0.02	0.01
3863-2	0.00	0.00	0.09	0.81	8.05	0.74	3.06	58.33	22.87	3.86	0.94	0.82	0.04	0.29	0.06	0.03
3863-2	0.00	0.00	0.13	19.27	15.52	0.42	2.89	40.66	16.82	2.47	0.91	0.68	0.02	0.17	0.02	0.01
3863-2	0.00	0.00	0.15	24.15	17.73	0.32	2.18	36.80	14.75	1.69	0.85	0.84	0.04	0.47	0.01	0.01
3863-2	0.00	0.00	0.19	25.37	17.25	0.25	2.66	32.97	17.44	1.67	0.94	0.78	0.01	0.45	0.00	0.01
3863-2	0.00	0.00	0.04	0.59	7.21	0.67	2.91	56.35	26.68	2.99	1.06	0.92	0.07	0.44	0.02	0.05
3863-2	0.00	0.00	0.20	27.82	18.08	0.37	2.56	33.69	13.30	1.77	0.97	0.68	0.02	0.51	0.01	0.03
3863-2	0.00	0.00	0.13	20.71	17.03	0.29	2.72	37.93	16.70	1.84	1.13	0.80	0.01	0.68	0.01	0.01
3863-2	0.00	0.00	0.17	26.25	17.87	0.22	2.26	37.01	12.61	1.48	0.85	0.82	0.05	0.41	0.01	0.00
3863-2	0.00	0.00	0.14	22.96	16.51	0.28	2.58	38.26	15.70	1.91	0.80	0.76	0.03	0.06	0.02	0.01
3863-2	0.00	0.00	0.15	22.04	16.77	0.20	2.61	40.01	14.57	1.96	0.81	0.71	0.04	0.11	0.02	0.01
3863-2	0.00	0.00	0.02	0.28	5.70	0.34	3.24	65.13	20.60	2.42	1.08	1.03	0.01	0.08	0.03	0.02
3863-5	0.00	0.00	0.17	23.40	16.42	0.41	2.44	32.08	21.06	2.40	0.80	0.61	0.02	0.14	0.02	0.02
3863-5	0.00	0.00	0.25	27.71	15.98	0.45	2.68	28.97	20.24	2.49	0.60	0.46	0.03	0.10	0.03	0.03
3863-5	0.00	0.00	0.20	28.26	17.16	0.32	2.23	31.84	16.72	1.68	0.74	0.68	0.03	0.13	0.01	0.01
3863-5	0.00	0.00	0.16	19.06	15.20	0.51	3.02	36.54	21.29	2.76	0.92	0.38	0.02	0.10	0.01	0.01
3863-5	0.00	0.00	0.03	0.29	6.06	0.37	3.26	53.48	31.80	2.74	0.78	0.88	0.05	0.18	0.04	0.03
3863-5	0.00	0.00	0.26	25.74	16.20	0.51	2.92	31.55	18.82	2.53	0.86	0.46	0.03	0.09	0.02	0.01
3863-5	0.00	0.00	0.19	20.65	15.48	0.38	2.76	35.90	20.56	2.54	0.78	0.61	0.06	0.06	0.01	0.02
3863-5	0.00	0.00	0.19	25.88	16.67	0.31	2.38	34.81	16.50	1.90	0.72	0.54	0.04	0.03	0.02	0.02

FIGURE 10C

SAMPLE	%8:0	%10:0	%12:0	%14:0	%16:0	%16:1	%18:0	%18:1	%18:2	%18:3	%20:0	%20:1	%20:2	%22:0	%22:1	%22:2
3863-5	0.00	0.00	0.20	29.58	16.88	0.31	2.01	28.68	18.97	1.82	0.62	0.69	0.03	0.17	0.01	0.02
3863-5	0.00	0.00	0.07	0.76	8.04	0.69	4.85	52.50	26.95	3.82	1.21	0.84	0.02	0.19	0.04	0.03
3863-5	0.00	0.00	0.14	16.17	14.15	0.57	3.81	37.23	23.14	3.08	0.98	0.53	0.03	0.09	0.02	0.04
3863-5	0.00	0.00	0.30	38.75	18.50	0.27	1.71	21.34	16.39	1.57	0.64	0.44	0.03	0.04	0.02	0.01

FIGURE 10D

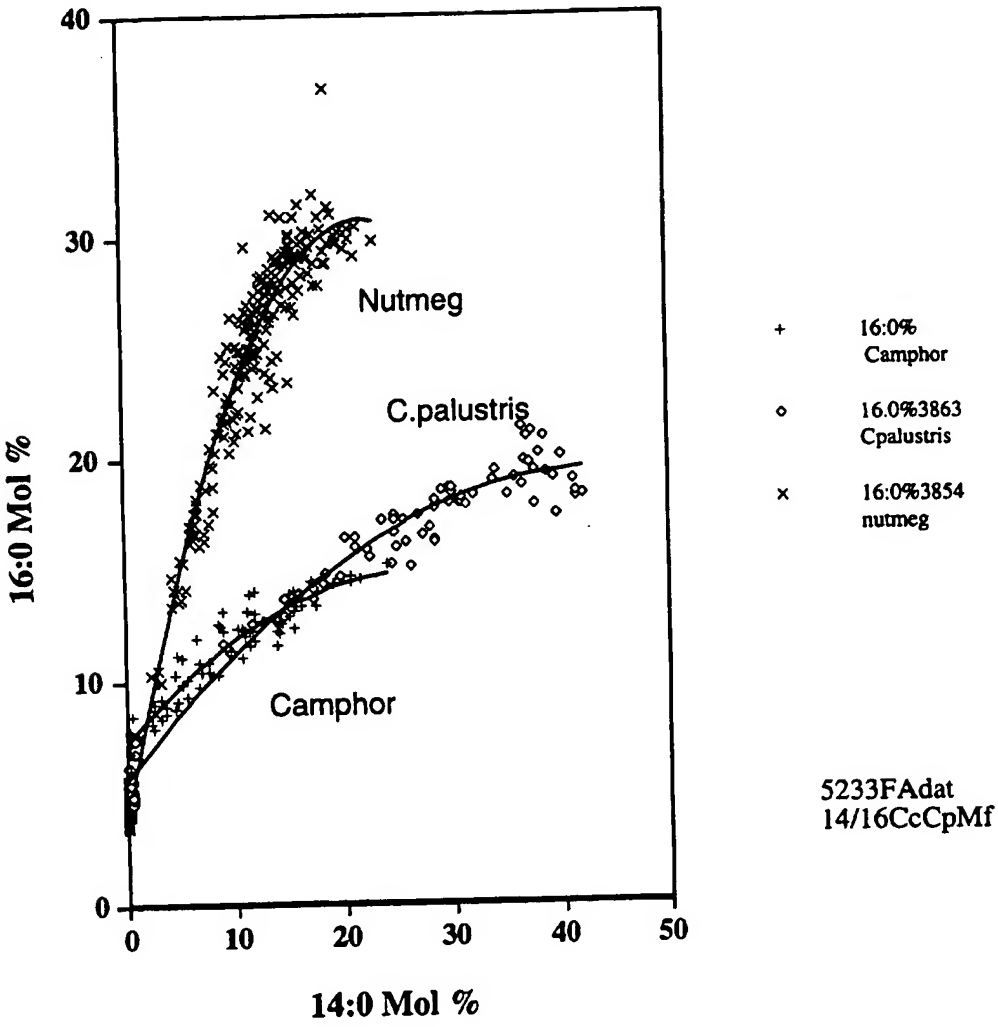
40
30
20
10
0
0
10
20
30
40
50
16:0 Mol %
14:0 Mol %
Nutmeg
C.palustris
Camphor
+ 16:0% Camphor
◇ 16.0%3863 Cpalustris
× 16:0%3854 nutmeg
5233FAdat
14/16CcCpMf

FIGURE 11

STRAIN_ID	8:0	10:0	12:0	14:0	16:0	16:1	18:0	18:1	18:2	18:3	20:0	20:1	20:2	22:0	22:1	22:2	24:0	24:1
3857-1	0	0.17	0.03	0.10	4.92	0.27	2.94	67.48	20.39	1.42	0.80	1.07	0.06	0.35	0	0	0	0
3857-2	0	0.16	0.25	10.94	23.01	0.73	5.74	37.57	17.82	1.19	1.48	0.59	0.02	0.49	0	0	0	0
3857-3	0	0.18	0.20	8.20	19.90	0.60	6.02	43.84	17.02	1.32	1.49	0.67	0.03	0.51	0	0	0	0
3857-4	0	0.18	0.23	11.15	28.00	0.94	5.44	30.86	19.46	1.44	1.37	0.47	0.00	0.46	0	0	0	0
3857-5	0	0.15	0.12	5.47	17.47	0.57	4.72	46.31	21.17	1.52	1.27	0.76	0.00	0.46	0	0	0	0
3857-7	0	0.16	0.14	5.00	14.03	0.53	4.29	52.91	19.24	1.39	1.11	0.79	0.01	0.40	0.01	0	0	0
3857-8	0	0.17	0.21	9.48	21.90	0.75	5.43	39.22	19.12	1.30	1.33	0.60	0.03	0.45	0	0	0	0
3857-9	0	0.15	0.19	8.65	20.70	0.63	5.57	42.80	17.57	1.27	1.37	0.64	0.01	0.45	0	0	0	0
3857-10	0	0.14	0.25	10.92	26.41	0.78	6.70	34.63	16.16	1.27	1.67	0.47	0.03	0.57	0.01	0	0	0
3857-11	0	0.16	0.14	5.75	17.17	0.63	5.04	46.43	20.68	1.46	1.31	0.70	0.04	0.49	0	0	0	0
3857-12	0	0.18	0.13	4.38	15.86	0.75	4.96	47.97	21.66	1.55	1.25	0.75	0.01	0.53	0.01	0	0	0
3857-13	0	0.17	0.18	7.18	18.93	0.67	5.29	43.03	20.70	1.40	1.28	0.67	0.04	0.45	0	0	0	0
3857-14	0	0.25	0.17	5.81	17.94	0.79	4.96	40.28	25.58	1.75	1.25	0.67	0.05	0.51	0	0	0	0
3857-15	0	0.20	0.13	4.52	14.83	0.63	4.21	47.22	24.45	1.58	1.03	0.74	0.05	0.39	0	0	0	0
3857-16	0	0.18	0.21	9.47	21.28	0.62	5.65	39.68	19.07	1.29	1.39	0.64	0.01	0.49	0	0	0	0
3857-17	0	0.17	0.13	5.62	17.52	0.60	4.88	47.62	19.75	1.35	1.19	0.71	0.04	0.43	0	0	0	0
3857-18	0	0.21	0.05	0.12	5.20	0.31	2.82	63.74	23.92	1.63	0.69	0.96	0.06	0.30	0	0	0	0
3857-19	0	0.18	0.17	6.95	19.06	0.69	5.24	43.48	20.57	1.37	1.22	0.65	0.01	0.42	0	0	0	0
3857-20	0	0.21	0.15	5.91	16.71	0.54	5.43	47.68	19.32	1.42	1.34	0.75	0.04	0.50	0	0	0	0
3864-2	0	0.19	0.28	23.17	20.08	0.33	2.08	27.83	22.17	1.69	0.67	0.80	0.08	0.33	0.28	0	0	0
3864-3	0	0.14	0.14	16.71	13.55	0.23	2.33	46.35	17.62	1.17	0.64	0.83	0.03	0.26	0	0	0	0
3864-4	0	0.19	0.08	3.12	6.89	0.31	2.67	61.32	22.05	1.47	0.65	0.91	0.06	0.28	0	0	0	0
3864-5	0	0.15	0.12	15.38	13.36	0.26	2.11	45.23	20.23	1.33	0.61	0.87	0.06	0.27	0.01	0	0	0
3864-6	0	0.12	0.14	17.86	14.65	0.30	1.90	38.82	23.07	1.48	0.56	0.78	0.07	0.25	0	0	0	0
3864-7	0	0.16	0.17	16.15	15.07	0.28	2.15	43.01	19.71	1.43	0.66	0.82	0.07	0.32	0	0	0	0
3864-8	0	0.14	0.20	22.94	18.12	0.24	2.04	34.27	19.13	1.23	0.62	0.74	0.06	0.26	0	0	0	0
3864-9	0	0.15	0.31	34.82	21.52	0.29	2.02	17.67	19.80	1.65	0.77	0.47	0.07	0.40	0.06	0	0	0
3864-10	0	0.11	0.16	21.21	15.67	0.25	1.72	35.98	22.00	1.32	0.53	0.75	0.06	0.24	0	0	0	0
3864-11	0	0.11	0.11	14.65	13.34	0.27	2.00	43.48	22.98	1.32	0.58	0.83	0.06	0.26	0	0	0	0
3864-16	0	0.13	0.14	17.73	14.18	0.26	1.98	40.29	22.37	1.35	0.55	0.76	0.01	0.24	0	0	0	0

FIGURE 12

INTERNATIONAL SEARCH REPORT

Interna[illegible]al Application No
PCT/US 96/01585

A. CLASSIFICATION OF SUBJECT MATTER
IPC 6 C12N15/82 C12N15/55 A01H5/00 C11B1/00

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
IPC 6 C12N A01H C11B

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
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Y	see page 24, line 29 - page 25, line 5 see page 32 - page 34 see page 32, line 32 - page 34, line 25 see figure 8 see figure 1 ---	4-6
X	WO,A,92 20236 (CALGENE INC) 26 November 1992	21
Y	see page 5, line 16 - line 28 see page 38, line 35 - page 40 see page 44, line 24 - page 50A see figure 5B; example 5 see figure 1A --- -/--	4-6

[X] Further documents are listed in the continuation of box C.

[X] Patent family members are listed in annex.

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"A" document defining the general state of the art which is not considered to be of particular relevance

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Date of the actual completion of the international search	Date of mailing of the international search report
25 September 1996	18. 10. 96

Name and mailing address of the ISA	Authorized officer
European Patent Office, P.B. 5818 Patentlaan 2 NL - 2280 HV Rijswijk Tel. (+31-70) 340-2040, Tx. 31 651 epo nl, Fax (+31-70) 340-3016	Maddox, A

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